

108203

From: Chan, Christina
Sent: Thursday, November 13, 2003 2:41 PM
To: Nguyen, Quang (AU1632); STIC-Biotech/ChemLib
Subject: RE: RUSH sequence search for 10/059720

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

CRFF

-----Original Message-----

From: Nguyen, Quang (AU1632)
Sent: Thursday, November 13, 2003 2:40 PM
To: Chan, Christina
Subject: RUSH sequence search for 10/059720

I would like to request for a rush sequence search for the above application, because it is an amended case due next-biweek.

Please search:

- (1) A nucleic acid encoding the amino acid sequence of SEQ ID NO:19; and
- (2) A nucleic acid of SEQ ID NO:18.

against commerical, pending and issued US Patent application databases.

I am in AU 1636, my mailbox is in CM1-11E12.

THANK YOU.

Point of Contact
P. Sheppard
Telephone number: (703) 308-4499

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 11/18/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
Copy-right (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2003, 23:00:45 / Search time 189 Seconds
(without alignments)
4284.022 Million cell updates/sec

Title: US-10-059-720-18

Perfect score: 300
Sequence: 1 CAGGAGCTACAGGCGAC.....CMAGGCTCCCTGTTAGCTT 300

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: N_Geneseq_190M03.*
2: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1990.DAT.*
3: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1981.DAT.*
4: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1982.DAT.*
5: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1983.DAT.*
6: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1984.DAT.*
7: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1985.DAT.*
8: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1986.DAT.*
9: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1987.DAT.*
10: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1988.DAT.*
11: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1990.DAT.*
12: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1991.DAT.*
13: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1992.DAT.*
14: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1993.DAT.*
15: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1994.DAT.*
16: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1995.DAT.*
17: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1996.DAT.*
18: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1997.DAT.*
19: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1998.DAT.*
20: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA1999.DAT.*
21: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA2000.DAT.*
22: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA2001.DAT.*
23: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA2002.DAT.*
24: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA2003.DAT.*
25: /SIDSI/5ggdata/Geneseq/Geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	294	90.0	294	18	ANT4348		CHW400-4Heptadfos
2	265.6	88.5	281	18	ANT4347		4Heptadfos protein
3	173.4	57.0	318	18	ANT4346		CHW500-Poab2FP (MO)
4	133.7	42.3	268	18	ANT4345		DNA encoding CHW50
5	130.8	43.6	1143	24	ABK0445		Human v-fos FBJ mu
6	130.8	43.6	2084	24	ABV4327		Breast carcinoma t
7	130.8	43.6	2084	24	ABV4327		Breast carcinoma t
8	130.8	43.6	2103	20	AZ41152		Human normal uteru

c	9	130.9	43.6	2180	24	AN054467
11	124.4	41.5	1946	22	AB47452	Human ovari ancl
12	124.4	41.5	1946	22	AB47452	Nucleotide sequen
13	124.4	41.5	1946	22	AB47452	Human foetal liver
14	124.4	41.5	1946	22	AB47452	Human foetal liver
15	124.4	41.5	1946	22	AB47452	Human brain expres
16	124.4	41.5	1946	22	AB47452	Probe #3420 for ge
17	124.4	41.5	1946	22	AB47452	Human brain expres
18	124.4	41.5	1946	22	AB47452	Probe #3442 for ge
19	124.4	41.5	1946	22	AB47452	Probe #3555 used t
20	124.4	41.5	1946	22	AB47452	Probe #3855 used t
21	124.4	41.5	1946	22	AB47452	Probe #1252 for g
22	124.4	41.5	1946	22	AB47452	Probe #1252 for g
23	124.4	41.5	1946	22	AB47452	Probe #1252 for g
24	124.4	41.5	1946	22	AB47452	Probe #1252 for g
25	124.4	41.5	1946	22	AB47452	Probe #1252 for g
26	124.4	41.5	1946	22	AB47452	Probe #1252 for g
27	124.4	41.5	1946	22	AB47452	Probe #1252 for g
28	124.4	41.5	1946	22	AB47452	Probe #1252 for g
29	124.4	41.5	1946	22	AB47452	Probe #1252 for g
30	124.4	41.5	1946	22	AB47452	Probe #1252 for g
31	124.4	41.5	1946	22	AB47452	Probe #1252 for g
32	124.4	41.5	1946	22	AB47452	Probe #1252 for g
33	124.4	41.5	1946	22	AB47452	Probe #1252 for g
34	124.4	41.5	1946	22	AB47452	Probe #1252 for g
35	124.4	41.5	1946	22	AB47452	Probe #1252 for g
36	124.4	41.5	1946	22	AB47452	Probe #1252 for g
37	124.4	41.5	1946	22	AB47452	Probe #1252 for g
38	123.4	41.1	3514	24	AKN04984	Human v-fos FBJ mu
39	123.4	41.1	3514	24	AKN04984	Human v-fos FBJ mu
40	123.4	41.1	3514	24	AKN04984	Human v-fos FBJ mu
41	123.4	41.1	3514	24	AKN04984	Human v-fos FBJ mu
42	123.4	41.1	3514	24	AKN04984	Human v-fos FBJ mu
43	123.4	41.1	3514	24	AKN04984	Human v-fos FBJ mu
44	123.4	41.1	3514	24	AKN04984	Human v-fos FBJ mu
45	123.4	41.1	3514	24	AKN04984	Human v-fos FBJ mu

ALIGNMENTS

RESULT 1
ID: 12-NOV-1997 (first entry)
ID: ANT4348 standard; DNA; 294 BP.
AC: ANT4348;
CT: 12-NOV-1997 (first entry)
CC: CHW400-4Heptadfos leucine zipper protein DNA.
DE: DNA binding protein; RNA binding protein; amphipathic peptide;
DE: acidic extension peptide; Gene control; gene regulation;
DE: transcription; dominant negative protein; c-fos; cancer;
DE: drug therapy; drug design; ss.
OS: ChimERIC Homo sapiens;
OS: ChimERIC bacteriophage phi-10;
OS: ChimERIC synthetic.
PM: MO9705249-A2
PP: 11-FEB-1997.
PP: 31-JUL-1996; 96NO-05312590.
PP: 31-JUL-1996; 96US-0001654.
PP: 31-JUL-1996; 96US-0001654.
PP: 23-MAY-1996; 96US-0018496.
XX: (KRYL/) KRYLOV D.
XX: (USFH) US DEPT HEALTH & HUMAN SERVICES.

PA (VINS//) VINSON C.R.
 KYxlow D, Vinson CR;
 XX
 XX
 DR NP1; 1997-145687/13.
 XX P-PSDB; AAM00949.
 XX
 DR New nucleic acid binding proteins - having an acidic amino acid
 FT sequence extension at the amino-terminus, to increase ability to
 PT regulate gene transcription, useful e.g. in cancer therapeutics
 XX
 PS Claim 16; Page 87; 144pp; English.
 XX
 XX This DNA sequence codes for ONV500-heptadFos leucine zipper
 CC includes an appended 4-heptad acidic extension. Claimed NABEs such
 CC as Fos having acidic peptide extensions are capable of regulating
 CC the function of a target nucleic acid or gene to which they are
 CC bound, and act as potent dominant-negative regulators of gene
 CC transcription, cell growth and cell proliferation. They can be
 CC used in cancer therapy, to treat diseases caused by eukaryotic
 CC microorganisms or by viruses, and as tools for drug development,
 CC rational drug design, and drug and gene therapies. They have an
 CC extended protein interaction surface or multimerization or
 CC dimerization interface that increases the stability of complexes
 CC formed.
 CC
 CC Sequence 294 BP; 96 A; 65 C; 88 G; 45 T; 0 other;
 XX
 XX Query March 98.04; Score 294; DB 18; Length 294;
 XX Best local similarity 100.04; Pred. No. 3.1e-68;
 XX Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 Qy 3 ATGGACTACAGAGAGAGATGACGATATGGCTATGATGATCTGTGACGCAATG 62
 Db 1 ATGGACTACAGAGAGAGATGACGATATGGCTATGATGATCTGTGACGCAATG 60
 XX
 Qy 63 GTTCGGATCTGATCTGAGCAAGCTGTGAGAACTGGCCCTGAAACGAGAGCTG 122
 Db 61 GTTCGGATCTGATCTGAGCAAGCTGTGAGAACTGGCCCTGAAACGAGAGCTG 120
 XX
 Qy 123 GAAAG 182
 Db 121 GAAAG 180
 XX
 Qy 183 CTGAG 242
 Db 181 CTGAG 240
 XX
 Qy 243 AAATAGAGTCTATCTGTGAGCACTGACGAGCTGCTGCAAGTCTCGATTAA 296
 Db 241 AAATAGAGTCTATCTGTGAGCACTGACGAGCTGCTGCAAGTCTCGATTAA 294
 XX
 RESULT 2
 AAT84347
 D AAT84347 standard; DNA; 281 BP.
 AC
 AC AAT84347;
 XX
 XX 11-NOV-1997 (first entry)
 XX
 DE (heptadFos protein DNA.
 XX
 XX DNA binding protein; RNA binding protein; amphipathic peptide;
 KW transcription; dominant negative protein; c-Fos; cancer;
 XX drug therapy; drug design; as.
 XX
 XX Chimeric Homo sapiens;
 OS Chimeric baculovirus phi-10;
 OS Chimeric synthetic.
 XX

FR Key Location/Qualifiers
 FT CDS 9..272
 FT T /tag= a
 XX
 XX MO9705249-A2.
 XX 13-FEB-1997.
 XX
 PF 31-JUL-1996; 96MC-US12590.
 XX
 XX 31-JUL-1996; 96US-0001654.
 XX 31-JUL-1996; 96US-0001654.
 XX 29-MAY-1996; 96US-0018456.
 XX
 XX (KRYLOW D, VINSON C.R.)
 XX (VINS//) VINSON C.R.
 XX KYxlow D, Vinson CR;
 XX
 XX NP1; 1997-145687/13.
 XX P-PSDB; AAM00949.
 XX
 XX New nucleic acid binding proteins - having an acidic amino acid
 FT sequence extension at the amino-terminus, to increase ability to
 PT regulate gene transcription, useful e.g. in cancer therapeutics
 XX
 XX Claim 16; Page 86; 144pp; English.
 XX
 XX This DNA sequence codes for theptadFos protein (AAM00949), a
 CC modified Fos nucleic acid binding protein (NABP) that includes
 CC an appended 4-heptad acidic extension. Claimed NABEs such as
 CC Fos having acidic peptide extensions are capable of regulating
 CC the function of a target nucleic acid or gene to which they are
 CC bound, and act as potent dominant-negative regulators of gene
 CC transcription, cell growth and cell proliferation. They can be
 CC used in cancer therapy, to treat diseases caused by eukaryotic
 CC microorganisms or by viruses, and as tools for drug development,
 CC rational drug design, and drug and gene therapies. They have an
 CC extended protein interaction surface or multimerization or
 CC dimerization interface that increases the stability of complexes
 CC formed.
 CC
 CC Sequence 281 BP; 90 A; 63 C; 80 G; 48 T; 0 other;
 XX
 XX Query March 88.57; Score 265.6; DB 18; Length 281;
 XX Best local similarity 98.54; Pred. No. 9.8e-61;
 XX Matches 268; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 XX
 Qy 25 ACAGCATATGCTAGCATGATCTGTGTCGACGCAATGCTGTGACTCTGCTGAC 84
 Db 1 ATATCATATGCTAGCATGATCTGTGTCGACGCAATGCTGTGACTCTGCTGAC 80
 XX
 Qy 85 AACCTCTGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 144
 Db 61 AACCTCTGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 140
 XX
 Qy 145 ACAGCAAG 204
 Db 121 ACAGCAAG 200
 XX
 Qy 205 TGTGTCGAG 264
 Db 181 TGTGTCGAG 260
 XX
 Qy 265 CTCACGAG 296
 Db 241 CTCACGAG 292
 XX
 RESULT 3
 AAT84346
 D AAT84346 standard; DNA; 318 BP.

XX 19-JUN-2000 (first entry)
 XX Human normal uterus tissue derived cDNA 28.
 DE Human; uterus; cancer; treatment; anticancer; cytostatic; gene therapy;
 XX AS7; expressed sequence tag, sp.
 XX
 XX Homo sapiens.
 XX
 XX DSI9817946-A1.
 XX
 XX 21-OCT-1999.
 XX
 XX 17-APR-1999, 98DE-1017946.
 XX
 XX 17-APR-1999; 98DE-1017946.
 XX
 XX (META-1) METAGEN GENES GENOFORSCHUNG MRH.
 XX
 XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;
 XX WP1; 1999-591956/S1.
 XX
 XX New nucleic acid sequences expressed in normal uterine tissues, and
 XX derived polypeptides, for treatment of uterine cancer and
 XX identification of therapeutic agents -
 XX
 XX Claim 3; Page 94; 154pp; German.
 XX
 XX This invention describes novel cDNA sequences (A) highly expressed in
 XX human normal uterine tissue, and polypeptides (B) having high activity
 XX and can be used for gene therapy. (A) are used (i) for recombinant
 XX expression of polypeptides (B) and (ii) to isolate complete genes.
 XX (B) are used (i) to identify agents suitable for treatment of uterine
 XX cancer and (ii) to isolate complete genes. (A) are used (i) for
 XX expression from gene therapy vectors and (ii) for generation of
 XX specific antibodies. (A) are identified by assembling ESTs (expressed
 XX sequence tags) from a particular tissue type before comparison of
 XX the sequence with the known sequence of the human uterus. (A) of the
 XX type to be revealed, so should reduce the number of failures associated
 XX with the fact that ESTs from different libraries may represent
 XX different parts of the same unknown gene, distorting the estimated
 XX frequency of the gene. (A) are used to identify agents suitable for
 XX treatment of the human uterine tissue derived cDNA fragments of the
 XX invention which encode the protein fragments represented in
 XX
 XX Sequence 2103 BP; 492 A; 573 C; 525 G; 513 T; 0 other;
 XX
 XX Query Match 43.6%; Score 130.8; DB 20; Length 2103;
 XX Best Local Similarity 92.0%; Pred. No. 7, 4e-25;
 XX Matches 139; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 XX
 XX QY 146 CGAGGAACCTGACTGAGGCGGAGACACACCTAGAGATGAGATCTGCTTT 205
 XX 588 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 647
 XX
 XX DY 206 CGAGCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 265
 XX 648 CGAGCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 707
 XX
 XX OY 266 TCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 295
 XX 708 TCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 737
 XX
 XX RESULT 9
 XX AB054467
 XX AB054467 standard; cDNA, 2180 BP.
 XX AC AB054467
 XX

22-AUG-2002 (first entry)
 XX Human ovarian antigen HTBV01 cDNA, SEQ ID NO:347.
 XX
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 XX ovarian cancer; breast cancer; tumour; reproductive system disorder;
 XX ovarian cancer; breast cancer; tumour; reproductive system disorder;
 XX PQOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 XX inflammatory condition; immune disorder; blood disorder;
 XX cardiovascular disorder; respiratory disorder; neurological disorder;
 XX cardiovascular disorder; respiratory disorder; neurological disorder;
 XX cardiovascular disorder; respiratory disorder; neurological disorder;
 XX gene therapy; chromosome mapping; forensic analysis; drug screening;
 XX gene therapy; chromosome mapping; forensic analysis; drug screening;
 XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 XX antineoplastic; immunomodulatory; neuroprotective; neuroprotective;
 XX antineoplastic; immunomodulatory; neuroprotective; neuroprotective;
 XX gene; 88.
 XX
 XX Homo sapiens.
 XX
 XX X0200200677-A1.
 XX
 XX 03-JUN-2002.
 XX
 XX 07-JUN-2001; 2001MO-081569.
 XX
 XX 07-JUN-2000; 2000US-209467P.
 XX
 XX (HMA-) HUMAN GENOME SCI INC.
 XX
 XX Birze CB, Rosen CA;
 XX
 XX WP1; 2002-147978/19.
 XX
 XX F-0005; AS414328.
 XX
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 XX useful in the prevention, treatment and diagnosis of cancer (e.g.
 XX ovarian cancer, breast cancer, tumour, reproductive system disorders and
 XX neurological diseases).
 XX
 XX Claim 1; SEQ ID NO 347; 292pp; English.
 XX
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 XX ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also
 XX encompasses polypeptides 908 identical and polynucleotides 955 identical
 XX to the sequences of the cDNAs. The invention also relates to the use of
 XX recombinant nucleic acid molecules and have cells comprising human ovarian antigen
 XX polynucleotides, antibodies against human ovarian antigens, and the use
 XX of ovarian antigen polynucleotides and polypeptides in diagnosing,
 XX treating, preventing or preventing ovarian cancer and breast cancer, and
 XX metastatic tumours of ovarian or breast origin, reproductive system
 XX disorders (e.g., infertility, disorders of pregnancy, anovulation,
 XX polycystic ovary syndrome, ovarian cysts and dysmenorrhea), ovarian
 XX cancer, breast cancer, tumour, reproductive system disorders, and toxic
 XX shock syndrome, inflammatory conditions (e.g., mastitis, oophoritis and
 XX vaginitis), immune disorders (e.g., congenital and acquired
 XX immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 XX reproductive system disorders, neurological disorders, gastrointestinal disorders
 XX and urinary system disorders. Ovarian antigen polypeptides and
 XX polynucleotides may also be used in screening for compounds which
 XX inhibit or enhance the biological activity of ovarian antigen polypeptides may
 XX further be used for gene therapy, chromosome mapping, in the
 XX identification of individuals and in forensic analysis, and the
 XX use of ovarian antigen polypeptides may be used as food additives or to prepare antibodies
 XX useful in disease diagnosis, drug screening and drug development. Present
 XX invention also represents cDNA encoding a human ovarian antigen of the
 XX
 XX Note: The sequence data for this patent did not form part of the printed
 XX specification, but was obtained in electronic format directly from WIPO
 XX at http://wipo.int/pat/publicated_pat_sequences.
 XX
 XX Sequence 2180 BP; 513 A; 596 C; 549 G; 519 T; 3 other;
 XX

Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 170 GAGAGGACCACTAGAAAGTGAAGAGTCTGCTTTCGACCGAGGATTCGCAACTGCT 229
DB 313 GAGAGGACCACTAGAAAGTGAAGAGTCTGCTTTCGACCGAGGATTCGCAACTGCT 372
QY 230 GAGAGGACCACTAGAAAGTGAAGAGTCTGCTTTCGACCGAGGATTCGCAACTGCT 289
DB 373 GAGAGGACCACTAGAAAGTGAAGAGTCTGCTTTCGACCGAGGATTCGCAACTGCT 432
QY 290 TGATTA 295
DB 433 TGATCA 438

```

RESULT 12

ABAS5207
ID ABAS5207 standard; DNA; 1946 BP.

AC ABAS5207;

XX 01-FEB-2002 (first entry)

DE Human foetal liver single exon nucleic acid probe #3512.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

OS Homo sapiens.

PN W0200157277-A2.

XX 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00669.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207455.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 27-SEP-2000; 2000US-0214667.

PR 04-OCT-2000; 2000US-0214659.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PN Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human foetal liver.

XX Claim 1, SEQ ID NO 3512; 639pp + sequence listing; English.

XX The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human
XX liver. The single exon nucleic acid probe may be used for predicting,
XX diagnosing, grading, staging, and monitoring diseases derived from human
XX foetal liver. The present sequence is a single exon nucleic acid
XX probe of the invention.

XX Note: The sequence data for this patent did not form part of the
XX human genome collection, but was obtained in electronic format directly
XX from WFO at fsp.wfo-inc./pub/published_pct_sequences.

XX Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 other;

```

Query Match 41.5%; Score 124.4; DB 22; Length 1946;
Best Local Similarity 95.2%; Pred. No. 3.5e-23;
Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 170 GAGAGGACCACTAGAAAGTGAAGAGTCTGCTTTCGACCGAGGATTCGCAACTGCT 229
DB 313 GAGAGGACCACTAGAAAGTGAAGAGTCTGCTTTCGACCGAGGATTCGCAACTGCT 372

```

```

QY 230 GAGAGGACCACTAGAAAGTGAAGAGTCTGCTTTCGACCGAGGATTCGCAACTGCT 289
DB 373 GAGAGGACCACTAGAAAGTGAAGAGTCTGCTTTCGACCGAGGATTCGCAACTGCT 432
QY 290 TGATTA 295
DB 433 TGATCA 438

```

RESULT 13

ABAS24954
ID ABAS24954 standard; DNA; 1946 BP.

XX ABAS24954;

XX 23-JAN-2002 (first entry)

DT Probe #3420 for gene expression analysis in human heart cell sample.

XX Human; gene expression; heart; microarray; vascular system; probe;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease; ss.

OS Homo sapiens.

PN W0200157274-A2.

XX 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00666.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207412.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 27-SEP-2000; 2000US-0214667.

PR 04-OCT-2000; 2000US-0214659.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PN Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488899/53.

XX Single exon nucleic acid probes for analyzing gene expression in human
XX hearts.

XX Claim 1, SEQ ID NO 3420; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart. The
XX present sequence is one such probe. The probes may be used for
XX predicting, diagnosing, grading, staging, and monitoring diseases derived
XX from the human heart via microarray. By measuring gene expression, the
XX probes are useful for predicting, diagnosing, grading, staging, and
XX monitoring and prognosing diseases of the human heart and vascular system
XX (congenital vascular disease, hypertension, cardiac arrhythmias and
XX other). The sequence data for this patent did not form part of the
XX specification, but was obtained in electronic format directly from WFO
XX at fsp.wfo-inc./pub/published_pct_sequences.

XX Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 other;

```

Query Match 41.5%; Score 124.4; DB 22; Length 1946;
Best Local Similarity 95.2%; Pred. No. 3.5e-23;
Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 170 GAGAGGACCACTAGAAAGTGAAGAGTCTGCTTTCGACCGAGGATTCGCAACTGCT 229
DB 313 GAGAGGACCACTAGAAAGTGAAGAGTCTGCTTTCGACCGAGGATTCGCAACTGCT 372

```

OY 230 GAAGGAGAGGAAAACCTAGAGTTCATCTCGACGCTCAGCGAGCTGCTCGAGATCC 289
 DB 373 GAAGGAGAGGAAAACCTAGAGTTCATCTCGACGCTCAGCGAGCTGCTCGAGATCC 432

OY 290 TGATTA 295
 DB 433 TGATGA 438

RESULT 14
 ID AK03468
 AC AK03468 standard; DNA; 1946 BP.
 AC AK03468;
 XX 05-NOV-2001 (first entry)
 XX Human brain expressed single exon probe SEQ ID NO: 3459.
 XX Human; brain expressed exon; gene expression analysis; probe;
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 XX epilepsy; cancer; ss.
 XX Homo sapiens.
 XX W0200157275-A2.
 XX 09-AUG-2001.
 XX 30-JUN-2001; 2001MO-US005667.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 03-AUG-2000; 2000US-0623468.
 XX 21-SEP-2000; 2000US-0234687.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000US-0024283.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human
 XX brain -
 XX Example 4; SEQ ID NO: 3459; 650pp + Sequence Listing; English.
 XX The present invention provides a number of single exon nucleic acid
 XX probes which are derived from genomic sequences expressed in the human
 XX brain. They can be used to measure gene expression in brain cell samples,
 XX which may enable the diagnosis and improved treatment of nervous system
 XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 XX epilepsy and cancer. The present sequence is one of the probes of the
 XX invention.
 XX Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 other;
 XX Query Match 41.5%; Score 124.4; DB 22; Length 1946;
 XX Best Local Similarity 99.2%; Pred. No. 3.5e-23;
 XX Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 170 GGAGCAGACCACTAGAGATGAGTTCGCTTCGACCGAGATTCGCACTGCT 229
 DB 313 GGAGCAGACCACTAGAGATGAGTTCGCTTCGACCGAGATTCGCACTGCT 372
 OY 230 GAAGGAGAGAAAACCTAGAGTTCATCTCGACGCTCAGCGATCC 289
 DB 373 GAAGGAGAGAAAACCTAGAGTTCATCTCGACGCTCAGCGATCC 432

OY 290 TGATTA 295
 DB 433 TGATGA 438

Search completed: November 16, 2003, 00:10:34
 Job time : 190 secs

OY 290 TGATTA 295
 DB 433 TGATGA 438

RESULT 15
 ID AK28922
 AC AK28922 standard; DNA; 1946 BP.
 AC AK28922;
 XX 06-NOV-2001 (first entry)
 XX Human bone marrow expressed single exon probe SEQ ID NO: 3479.
 XX Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
 XX Homo sapiens.
 XX W0200157276-A2.
 XX 09-AUG-2001.
 XX 30-JUN-2001; 2001MO-US005668.
 XX 04-FEB-2000; 2000US-0180312.
 XX 26-MAY-2000; 2000US-0207456.
 XX 03-AUG-2000; 2000US-0623468.
 XX 21-SEP-2000; 2000US-0234687.
 XX 27-SEP-2000; 2000US-0236359.
 XX 04-OCT-2000; 2000US-0024283.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for
 XX analyzing gene expression in human bone marrow -
 XX Example 4; SEQ ID NO: 3479; 650pp + Sequence Listing; English.
 XX The present invention provides a number of single exon nucleic acid
 XX probes which are derived from genomic sequences expressed in the human
 XX bone marrow. They can be used to measure gene expression in bone marrow
 XX samples, which may enable the diagnosis and improved treatment of bone marrow
 XX diseases such as lymphoma, leukaemia and myeloma. The present sequence is one of
 XX the probes of the invention.
 XX Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 other;
 XX Query Match 41.5%; Score 124.4; DB 22; Length 1946;
 XX Best Local Similarity 99.2%; Pred. No. 3.5e-23;
 XX Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 170 GGAGCAGACCACTAGAGATGAGTTCGCTTCGACCGAGATTCGCACTGCT 229
 DB 313 GGAGCAGACCACTAGAGATGAGTTCGCTTCGACCGAGATTCGCACTGCT 372
 OY 230 GAAGGAGAGAAAACCTAGAGTTCATCTCGACGCTCAGCGATCC 289
 DB 373 GAAGGAGAGAAAACCTAGAGTTCATCTCGACGCTCAGCGATCC 432

OY 290 TGATTA 295
 DB 433 TGATGA 438

Search completed: November 16, 2003, 00:10:34
 Job time : 190 secs

Mon Nov 17 10:02:12 2003

us-10-059-720-18.rng

Page 10

B0082970
 E002970.1 GI:19941116
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Cetartihini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 326)
 Kim M.S., Hahn Y., Oh J.H., Lee J.Y., Ahn H.Y., Chu M.Y., Kim M.R.,
 Oh K.J., Cheong J.E., Sohn H.Y., Kim J.M., Park H.S., Kim S. and
 J.C. Frontier Korean EST Project 2001
 JOURNAL
 COMMENT
 Unpublished
 Contact: Kim YS
 Genomic Research
 52 Boun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: 42-42-860-4470
 Fax: 42-42-860-4469 kribb@kr.ac.kr
 Plate: 59 row: P column: 11
 High quality sequence stop: 326.
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_line="SK402"
 /lab_host="top10P"
 /clone_lib="SK402"
 Site 3: Not: The poly (A)- RNA was denatured/labeled with
 bacterial alkaline phosphatase (BAP) and then dephosphorylated with
 with tobacco acid pyrophosphatase (TAP). The dephosphorylated
 primer was ligated to the RNA. The RNA library was constructed by
 insert by ligation. The RNA library was constructed by ligation
 cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 50% of the cDNA vector was
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-berg method. The
 obtained cDNA vectors were used for transformation of
 the cDNA libraries constructed by this method are
 full-length enriched cDNA library."
 BASE COUNT 99 a 74 c 100 g 53 t
 ORIGIN
 Query Match 43.6%; Score 130.8; DB 13; Length 326;
 Best Local Similarity 92.0%; Pred. No. 1.2e-21;
 Matches 138; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
 QY 146 GCGAGAAACCTGAACTCGAGCGGAGAGACCACTAGAGATGAGAGTCTCTTT 205
 DB 123 GAGCTGCTGATCTCTGAGCGGAGAGACCACTAGAGATGAGAGTCTCTTT 182
 QY 206 GCGAGCGGAGAGTCTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 265
 DB 183 GCGAGCGGAGAGTCTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 242
 QY 266 TCACCGAGTCTGCGAGAGTCTGAGTCTGATTA 295
 DB 243 TCACCGAGTCTGCGAGAGTCTGAGTCTGATTA 272
 RESULT 7
 AM881177 337 bp mRNA linear EST 23-MAY-2000
 LOCUS
 C0007003.1-170400-197-02 OT0033 Homo sapiens cDNA, mRNA sequence..
 ACCESSION
 AM881177
 VERSION
 AM881177.1 GI:18043187

EST.
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Cetartihini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 337)
 Cortes, R., Verjovsky-Almeida, S., Briones, M.R.,
 Balsa, M., G. Gallo, M., Matsuoka, A., Bain, G.S., Costa, P.,
 Goldman, G.H., Carvalho, A.F.P., Zago, A., Salas, G.S., Simpson, D.H.,
 Brunstein, A., de Oliveira, S., Bucher, P., Jongeneel, C.V., O'Hare
 M.J.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 C. Frontiers in Molecular Biology and Medicine
 Shotgun sequencing of the human transcriptome with OAR expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL
 COMMENT
 Unpublished
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 1000 University Avenue
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: 55-11-2704922
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 400-157-02425300-0-176421
 Seq primer: puc 18 forward
 High quality sequence stop: 337.
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="OT0033"
 /note="Organ: ovary; Vector: puc18; Site 1: SmaI; Site 2:
 SmaI; A mini-library was made by cloning products derived
 from the human transcriptome into the puc18 vector. The library
 716 - Ludwig Institute for Cancer Research profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions.
 BASE COUNT 101 a 74 c 103 g 59 t
 ORIGIN
 Query Match 43.6%; Score 130.8; DB 10; Length 337;
 Best Local Similarity 92.0%; Pred. No. 1.2e-21;
 Matches 138; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 QY 146 GCGAGAAACCTGAACTCGAGCGGAGAGACCACTAGAGATGAGAGTCTCTTT 205
 DB 122 GAGCTGCTGATCTCTGAGCGGAGAGACCACTAGAGATGAGAGTCTCTTT 181
 QY 206 GCGAGCGGAGAGTCTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 265
 DB 182 GCGAGCGGAGAGTCTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 241
 QY 266 TCACCGAGTCTGCGAGAGTCTGAGTCTGATTA 295
 DB 242 TCACCGAGTCTGCGAGAGTCTGAGTCTGATTA 271
 RESULT 8
 BF829872 386 bp mRNA linear EST 13-JAN-2001
 LOCUS
 M3-INO052-261200-002-d11 IN0052 Homo sapiens cDNA, mRNA sequence..
 ACCESSION
 BF829872.1 GI:12175899
 KEYWORDS
 EST.
 Homo sapiens (human)


```

BASE COUNT
ORIGIN
146 a      161 c      161 g
/mol_type="mRNA"
/job_xref=taxon:9606"
/sex="Male and Female"
/tissue_type="Adipose"
/clone_lib="Human Fat"
/ncbi_vector= lambda

```

[illegible]

Search completed: November 16, 2003, 00:57:56
Job time : 1319 secs

GenCore version 5.1.6
Copyright (C) 1995 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2003, 00:58:11 ; Search time 204 Seconds

4806.183 Million cell updates/sec

Title: US-10-059-720-18

Perfect score: 300

Sequence: 1 CATGAGTACATCAGGAGAC.....CAGATCCCTCATTAAGCTT 300

Scoring table: IDENTITY: NUC

Gapop 10.0 ; Gapext 1.0

Searched: 2169961 seqs, 1634102185 residues

Total number of hits satisfying chosen parameters: 4339922

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/prodata/1/pubnra/US07_PUBCOMB.seq.*

2: /cgn2_6/prodata/1/pubnra/US06_PUBCOMB.seq.*

3: /cgn2_6/prodata/1/pubnra/US05_PUBCOMB.seq.*

4: /cgn2_6/prodata/1/pubnra/US04_PUBCOMB.seq.*

5: /cgn2_6/prodata/1/pubnra/US03_PUBCOMB.seq.*

6: /cgn2_6/prodata/1/pubnra/US02_PUBCOMB.seq.*

7: /cgn2_6/prodata/1/pubnra/US01_PUBCOMB.seq.*

8: /cgn2_6/prodata/1/pubnra/US00_PUBCOMB.seq.*

9: /cgn2_6/prodata/1/pubnra/US09_PUBCOMB.seq.*

10: /cgn2_6/prodata/1/pubnra/US08_PUBCOMB.seq.*

11: /cgn2_6/prodata/1/pubnra/US07_PUBCOMB.seq.*

12: /cgn2_6/prodata/1/pubnra/US06_PUBCOMB.seq.*

13: /cgn2_6/prodata/1/pubnra/US05_PUBCOMB.seq.*

14: /cgn2_6/prodata/1/pubnra/US04_PUBCOMB.seq.*

15: /cgn2_6/prodata/1/pubnra/US03_PUBCOMB.seq.*

16: /cgn2_6/prodata/1/pubnra/US02_PUBCOMB.seq.*

17: /cgn2_6/prodata/1/pubnra/US01_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	300	100.0	300 14 US-10-059-720-18	Sequence 18, Appl
2	267.2	89.1	281 14 US-10-059-720-18	Sequence 16, Appl
3	267.2	89.1	281 14 US-10-059-720-18	Sequence 14, Appl
4	170.6	57.5	265 14 US-10-059-720-18	Sequence 15, Appl
5	133.4	44.5	262 14 US-10-059-720-12	Sequence 12, Appl
6	130.8	43.6	426 11 US-09-918-995-33976	Sequence 33976, A
7	110.8	43.6	2195 12 US-09-918-995-33976	Sequence 33976, A
8	110.8	43.6	2195 12 US-09-918-995-33976	Sequence 33976, A
9	130.2	43.4	273 14 US-10-070-676-16	Sequence 16, Appl
10	127.6	42.5	435 11 US-09-918-995-37466	Sequence 37466, A
11	127.6	42.5	435 11 US-09-918-995-37466	Sequence 37466, A
12	127.6	42.5	435 11 US-09-918-995-37466	Sequence 37466, A
13	124.4	41.5	496 12 US-10-029-386-25813	Sequence 25813, A
14	124.4	41.5	600 12 US-10-029-386-12113	Sequence 12113, A
15	124.4	41.5	1346 9 US-09-864-761-3420	Sequence 3420, Ap
16	124.4	41.5	2227 13 US-10-002-600-39	Sequence 39, Appl

17 124.4 41.5 3565 12 US-09-873-319-649
 18 124.4 41.5 3565 12 US-09-860-706-993
 19 124.4 41.5 3565 12 US-09-873-3670-793
 20 124.4 41.5 3565 12 US-09-873-3670-793
 21 124.4 41.5 3565 12 US-09-873-3670-793
 22 124.4 41.5 3565 12 US-09-864-761-20191
 23 124.4 41.5 3565 12 US-09-864-761-20191
 24 124.4 41.5 3565 12 US-09-864-761-20191
 25 124.4 41.5 3565 12 US-09-864-761-20191
 26 124.4 41.5 3565 12 US-09-864-761-20191
 27 124.4 41.5 3565 12 US-09-864-761-20191
 28 124.4 41.5 3565 12 US-09-864-761-20191
 29 124.4 41.5 3565 12 US-09-864-761-20191
 30 124.4 41.5 3565 12 US-09-864-761-20191
 31 124.4 41.5 3565 12 US-09-864-761-20191
 32 124.4 41.5 3565 12 US-09-864-761-20191
 33 124.4 41.5 3565 12 US-09-864-761-20191
 34 124.4 41.5 3565 12 US-09-864-761-20191
 35 124.4 41.5 3565 12 US-09-864-761-20191
 36 124.4 41.5 3565 12 US-09-864-761-20191
 37 124.4 41.5 3565 12 US-09-864-761-20191
 38 124.4 41.5 3565 12 US-09-864-761-20191
 39 124.4 41.5 3565 12 US-09-864-761-20191
 40 124.4 41.5 3565 12 US-09-864-761-20191
 41 124.4 41.5 3565 12 US-09-864-761-20191
 42 124.4 41.5 3565 12 US-09-864-761-20191
 43 124.4 41.5 3565 12 US-09-864-761-20191
 44 124.4 41.5 3565 12 US-09-864-761-20191
 45 124.4 41.5 3565 12 US-09-864-761-20191

ALIGNMENTS

RESULTS

Result 1 is 720-18

Sequence 18, Application US10059720

Publication No. US2003002731A1

GENERAL INFORMATION:

INVENTOR: KAYLOV, ITAY

ATTORNEY: KAYLOV, ITAY

TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN

INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF A

CELLULAR PROTEIN

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

ATTORNEY: MORGAN & FINNEGAN, L.L.P.

CITY: New York

STATE: NY

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: MS WORD 97

SEQUENCE SCHEMATIC:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/059-720

PRIOR APPLICATION NUMBER: 60/001-654

FILING DATE: 31 JUL-1995

APPLICATION NUMBER: 60/018-496

SEQUENCE NUMBER: 60/018-496

APPLICATION NUMBER: 60/018-496

FILING DATE: 31 JULY-1996

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 35,353

REFERENCE/DOCKET NUMBER: 2026-419982

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)758-4800

REGISTRATION NUMBER: 35,353
 REFERENCE/DOCKET NUMBER: 2026-419052
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 FAX: (212) 758-4849
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 324 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 US-10-059-720-14
 Query Match
 Best Local Similarity 59.8%; Score 179.4; DB 14; Length 324;
 Matches 250; Conservative 0; Mismatches 46; Indels 26; Gaps 2;
 QY 1 CCAAGTACCTGACAGGACGACGACAGCATATGCTAGCATGACTGTGGACGACAAA 60
 DB 1 CAGTGTCTACAGGACGACGACGACGACGACGACGACGACGACGACGACGACG 60
 QY 61 TGGTGTGGGATCTCTTCTGACGACACGTGTGGGAACTGTGGCCCTGAAACGAGAGC 120
 DB 61 TGGTGTGGGATCTCTTCTGACGACACGTGTGGGAACTGTGGCCCTGAAACGAGAGC 120
 QY 121 TGGTGTGGGATCTCTTCTGACGACGATCTCTTCCAGAGGAG-AGTGGACAGAGATC 119
 QY 121 TGGTGTGGGATCTCTTCTGACGACGATCTCTTCCAGAGGAG-AGTGGACAGAGATC 115
 DB 120 CAGAGGAGAGAGATATAGATGTGCTGTGCGCAATGTGCCACGAGAGAGGCTGACT 179
 QY 156 GCTGAAGTCTGGGACGACGACGACGACGACGACGACGACGACGACGACGACG 215
 DB 156 GCTGAAGTCTGGGACGACGACGACGACGACGACGACGACGACGACGACGACG 215
 QY 180 GATACATCTCCAGGACGACGACGACGACGACGACGACGACGACGACGACGAC 239
 QY 216 ATTGCCAATCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 275
 DB 240 ATTGCCAATCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 299
 QY 276 GCTCGAGAGGCTCGGTGTATAGCTT 300
 DB 300 GCTCGAGAGGCTCGGTGTATAGCTT 324

RESULT 4
 US-10-059-720-10
 Sequence 10, Application US/10059720
 Publication No. US20030027314A1
 GENERAL INFORMATION:
 APPLICANT: VINCOW, Charles R.
 TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN
 INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF A
 CELLULAR PROTEIN
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 STREET: 345 Park Avenue
 CITY: New York
 STATE: NY
 ZIP: 10154-0053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/059,720
 PRIORITY NUMBER: 2002
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/001,654
 FILING DATE: 31-JUL-1995

APPLICATION NUMBER: 60/018,496
 FILING DATE: 31-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Serunian, Leslie A.
 REGISTRATION NUMBER: 35,353
 REFERENCE/DOCKET NUMBER: 2026-419052
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 FAX: (212) 758-4849
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 266 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-10-059-720-10
 Query Match
 Best Local Similarity 53.5%; Score 160.6; DB 14; Length 266;
 Matches 163; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CAGTGTCTACAGGACGACGACGACGACGACGACGACGACGACGACGACGACG 60
 DB 1 CAGTGTCTACAGGACGACGACGACGACGACGACGACGACGACGACGACGACG 60
 QY 61 TGGTGTGGGATCTCTTCTGACGACGATCTCTTCCAGAGGAG-AGTGGACAGAGATC 120
 DB 61 TGGTGTGGGATCTCTTCTGACGACGATCTCTTCCAGAGGAG-AGTGGACAGAGATC 120
 QY 121 TGGTGTGGGATCTCTTCTGACGACGATCTCTTCCAGAGGAG-AGTGGACAGAGATC 167
 DB 121 TGGTGTGGGATCTCTTCTGACGACGATCTCTTCCAGAGGAG-AGTGGACAGAGATC 167

RESULT 5
 US-10-059-720-12
 Sequence 12, Application US/10059720
 Publication No. US20030027314A1
 GENERAL INFORMATION:
 APPLICANT: VINCOW, Charles R.
 TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN
 INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF A
 CELLULAR PROTEIN
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 STREET: 345 Park Avenue
 CITY: New York
 STATE: NY
 ZIP: 10154-0053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/059,720
 PRIORITY NUMBER: 2002
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/001,654
 FILING DATE: 31-JUL-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Serunian, Leslie A.

REGISTRATION NUMBER: 35,353
 TELEPHONE: 2026-4199052
 TELEFAX: (212)759-4800
 INFORMATION: (212)751-6849
 SEQUENCE CHARACTERISTICS:
 LENGTH: 262 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: unknown
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Query Match 44.5%; Score 133.4; DB 14; Length 262;
 Best Local Similarity 92.7%; Pred. No. 4,7e-30;
 Matches 140; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
 QY 146 GCGAAGAACTCTGAATCTCGAGCGGAGACCACTAGAGATGAGAGTCTGTTT 205
 DB 103 GAGCTGATCTATCACTCTCAAGCGGAGACCACTAGAGATGAGAGTCTGTTT 162
 QY 206 GCGACGAGATTCCTCACTCTGAGGAGAGAGAACTAGAGTTCATCTGCAGC 265
 DB 163 GCGACGAGATTCCTCACTCTGAGGAGAGAGAACTAGAGTTCATCTGCAGC 222
 QY 266 TCACGACCTCTGTCAGATCTCCCTGATTA 296
 DB 223 TCACGACCTCTGTCAGATCTCCCTGATTA 253

RESULT 6

US-09-918-995-133976
 Sequence 33976, Application US/09918995
 GENERAL INFORMATION: v-fos id; murine oncosarcoma viral oncogene
 APPLICANT: Byseq, Inc.
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 FROM THE GENOMIC DNA OF A MURINE ONCOSARCOMA CELL LINE
 FILE REFERENCE: 20411-755
 CURRENT APPLICATION NUMBER: US/09/918-995
 CURRENT FILING DATE: 2001-07-30
 PRIOR FILING DATE: 1999-01-28
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 133976
 SEQ LENGTH: 426
 TYPE: DNA
 ORGANISM: Homo sapiens

US-09-918-995-133976
 Query Match 43.6%; Score 130.8; DB 11; Length 426;
 Best Local Similarity 92.0%; Pred. No. 3.2e-29;
 Matches 138; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 QY 146 GCGAAGAACTCTGAATCTCGAGCGGAGACCACTAGAGATGAGAGTCTGTTT 205
 DB 149 GAGCTGATCTATCACTCTCAAGCGGAGACCACTAGAGATGAGAGTCTGTTT 208
 QY 206 GCGACGAGATTCCTCACTCTGAGGAGAGAGAACTAGAGTTCATCTGCAGC 265
 DB 209 GCGACGAGATTCCTCACTCTGAGGAGAGAGAACTAGAGTTCATCTGCAGC 268
 QY 266 TCACGACCTCTGTCAGATCTCCCTGATTA 295
 DB 269 TCACGACCTCTGTCAGATCTCCCTGATTA 298

RESULT 7

US-10-007-926A-318
 Sequence 318, Application US/10007926A

Publication NO. US2003014339A1
 GENERAL INFORMATION: FRANCIS
 APPLICANT: BOURGATTE, REMI
 APPLICANT: BIRNBAUM, DANIEL
 APPLICANT: NGUYEN, CATHERINE
 APPLICANT: NGUYEN, VINCENT
 APPLICANT: PERRY, VINCENT
 TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
 TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
 CURRENT APPLICATION NUMBER: US/10/007,926A
 PRIOR FILING DATE: 2001-12-07
 PRIOR FILING DATE: 2000-02-08
 NUMBER OF SEQ ID NOS: 68
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 318
 LENGTH: 2084
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: v-fos id; murine oncosarcoma viral oncogene
 APPLICANT: BOURGATTE, REMI
 US-10-007-926A-318

Query Match 43.6%; Score 130.8; DB 12; Length 2084;
 Best Local Similarity 92.7%; Pred. No. 4.7e-30;
 Matches 138; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 QY 146 GCGAAGAACTCTGAATCTCGAGCGGAGACCACTAGAGATGAGAGTCTGTTT 205
 DB 612 GAGCTGATCTATCACTCTCAAGCGGAGACCACTAGAGATGAGAGTCTGTTT 691
 QY 206 GCGACGAGATTCCTCACTCTGAGGAGAGAGAACTAGAGTTCATCTGCAGC 265
 DB 692 GCGACGAGATTCCTCACTCTGAGGAGAGAGAACTAGAGTTCATCTGCAGC 751
 QY 266 TCACGACCTCTGTCAGATCTCCCTGATTA 295
 DB 752 TCACGACCTCTGTCAGATCTCCCTGATTA 298

US-09-971-132-8
 Sequence 8, Application US/09971132
 Publication NO. US2003013428A1
 GENERAL INFORMATION: David P.
 APPLICANT: Pearson, Cecelia I.
 APPLICANT: Cocks, Benjamin G.
 TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION
 CURRENT APPLICATION NUMBER: US/09/971,132
 PRIOR FILING DATE: 2001-10-03
 PRIOR FILING DATE: 2001-03-03
 NUMBER OF SEQ ID NOS: 10-03
 SOFTWARE: PERL Program
 SEQ ID NO 8
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Template ID: 899156.22
 US-09-971-132-8

Query Match 43.6%; Score 130.8; DB 12; Length 2135;
 Best Local Similarity 92.7%; Pred. No. 4.7e-30;
 Matches 138; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 QY 146 GCGAAGAACTCTGAATCTCGAGCGGAGACCACTAGAGATGAGAGTCTGTTT 205

; PRIOR APPLICATION NUMBER: IL 125456
 ; PRIOR FILING DATE: 1998-07-22
 ; PRIOR FILING DATE: 1999-01-12
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.1
 ; SEQUENCE LENGTH: 435
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-765-298A-1

Query Match 41.5%; Score 124.4; DB 10; Length 435;
 Best Local Similarity 99.21; Pred. No. 2.6e-27;
 Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 170 GGAGCAGACCACTAGAGAGAGAGTCTGTTTGGACCGAGAGTCCCACTGCT 229
 Db 219 GGAGCAGACCACTAGAGAGAGAGTCTGTTTGGACCGAGAGTCCCACTGCT 278
 QY 210 GGAGCAGAGAAAATAGAGTCTCTGGAGCTCAGCAGCTGCTGGAAGATCC 289
 Db 279 GGAGCAGAGAAAATAGAGTCTCTGGAGCTCAGCAGCTGCTGGAAGATCC 338
 QY 290 TGATTA 295
 Db 339 TGATTA 344

RESULT 13

US-10-029-386-25813
 ; Sequence 12113, Application US/10029386
 ; Publication No. US20030194704A1
 ; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: AECMICA-X-2 US/10/023,386
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 34288
 ; SOFTWARE: Anthonax Sequence Listing Engine vers. 1.1
 ; SEQUENCE LENGTH: 436
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: MAP TO CHR14.3
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 19
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 277
 ; OTHER INFORMATION: EST HUMAN HIT: B1908747.1, EVALUATE 0.008e+00
 ; OTHER INFORMATION: SMITSPROT HIT: P01100, EVALUATE 8.00e-87
 ; OTHER INFORMATION: NT HIT: AF111167.2, EVALUATE 0.00e+00

US-10-029-386-25813
 Query Match 41.5%; Score 124.4; DB 12; Length 436;
 Best Local Similarity 99.21; Pred. No. 2.7e-27;
 Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 170 GGAGCAGACCACTAGAGAGAGAGTCTGTTTGGACCGAGAGTCCCACTGCT 229
 Db 1 GGAGCAGACCACTAGAGAGAGAGTCTGTTTGGACCGAGAGTCCCACTGCT 60
 QY 210 GGAGCAGAGAAAATAGAGTCTCTGGAGCTCAGCAGCTGCTGGAAGATCC 289
 Db 61 GGAGCAGAGAAAATAGAGTCTCTGGAGCTCAGCAGCTGCTGGAAGATCC 120
 QY 290 TGATTA 295
 Db 121 TGATTA 126

RESULT 14

US-10-029-386-12113
 ; Sequence 12113, Application US/10029386
 ; Publication No. US20030194704A1
 ; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: AECMICA-X-2 US/10/029,386
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 34288
 ; SOFTWARE: Anthonax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 12113
 ; LENGTH: 600
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO CHR14.3
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 19
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 27
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.9
 ; OTHER INFORMATION: NT HIT: AF111167.2, EVALUATE 0.00e+00
 ; OTHER INFORMATION: SMITSPROT HIT: P01100, EVALUATE 8.00e-84
 ; OTHER INFORMATION: EST_HUMAN HIT: B526890.1, EVALUATE 0.00e+00

US-10-029-386-12113

Query Match 41.5%; Score 124.4; DB 12; Length 600;
 Best Local Similarity 99.21; Pred. No. 2.9e-27;
 Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 170 GGAGCAGACCACTAGAGAGAGAGTCTGTTTGGACCGAGAGTCCCACTGCT 229
 Db 69 GGAGCAGACCACTAGAGAGAGAGTCTGTTTGGACCGAGAGTCCCACTGCT 128
 QY 210 GGAGCAGAGAAAATAGAGTCTCTGGAGCTCAGCAGCTGCTGGAAGATCC 289
 Db 129 GGAGCAGAGAAAATAGAGTCTCTGGAGCTCAGCAGCTGCTGGAAGATCC 188
 QY 290 TGATTA 295
 Db 189 TGATTA 194

RESULT 15

US-09-864-761-3420
 ; Sequence 3420, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
 ; FILE REFERENCE: Aecmica-X-1 US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666

```

/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
/ SEQ ID NO: 1946
/ LENGTH: 1946
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ SEQUENCE INFORMATION: MAP TO AF11167.2
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.2
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.4
/ OTHER INFORMATION: EXPRESSED IN HUMAN SPERM, SIGNAL = 5.2
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
/ OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.5
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
/ OTHER INFORMATION: EXPRESSED IN HUMAN SPERM, SIGNAL = 1.8
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
US-09-864-761-3420

```

```

Query Match 41.5%; Score 124.4; DB 9; Length 1946;
L Similarity 95.2%; Pred No. 4.1e-27;
Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 170 CGAGCGAGCACTTACAGAGTGGAGTCTGCTTCGAGCGAGCATTCGCACTGCT 229
Db 313 CGAGGAGCACTTACAGAGTGGAGTCTGCTTCGAGCGAGCATTCGCACTGCT 372
Oy 230 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 289
Db 373 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
Oy 290 TGATTA 295
Db 433 TATCA 438

Search completed: November 16, 2003, 01:36:23
Job time : 205 secs

```



```

Query Match          98.0%; Score 294; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.4e-71;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 ATGAGCTACAGAGAGACAGTACAGCATATGCTAGCATCTGCTGGACAGCAATG 62
DB  1 ATGAGCTACAGAGAGACAGTACAGCATATGCTAGCATCTGCTGGACAGCAATG 60
QY  63 GTGGTGGGATCTTCTGACTGGAACACATGCTGAGCAAGTGGCCCTGAAAAGAGAGCTG 122
DB  61 GTGGTGGGATCTTCTGACTGGAACACATGCTGAGCAAGTGGCCCTGAAAAGAGAGCTG 120
QY  123 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 182
DB  121 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY  183 CTAGAGAGTGAAGATCTCTCTTCTGGACAGCGGATTCGCAACCTGCTGAGGAGAGCA 242
DB  181 CTAGAGAGTGAAGATCTCTCTTCTGGACAGCGGATTCGCAACCTGCTGAGGAGAGCA 240
QY  243 AACTAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 296
DB  241 AACTAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 294

RESULT 3
US-05-239-495F-16
; Sequence 16, Application US/09299495F
; Patent No. 6361968
; GENETIC INFORMATION:
; APPLICANT: VINSON, Charles R.
; APPLICANT: KRYLOV, Dmitry
; TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN
; COMPLEXITY SPACE TO INACTIVATE THE FUNCTION OF A
; CELLULAR PROTEIN
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 445 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS WORD 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,495F
; FILING DATE: 26-Apr-1999
; PRIOR APPLICATION NUMBER: 60/001,654
; APPLICATION NUMBER: 60/001,654
; FILING DATE: 31-JUL-1995
; APPLICATION NUMBER: 60/018,496
; FILING DATE: 29-MAY-1996
; APPLICATION NUMBER: 60,011
; FILING DATE: 31-JULY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Serunian, Leslie A.
; ADDRESS: 35-353
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 2026-4199US2
; TELEPHONE: (212)758-4800
; INFORMATION FOR SEQ ID NO: 16:
; SEQ ID NO: 16: 294
; LENGTH: 294 base pairs
; TYPE: nucleic acid
; ORIGIN: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Query Match          100.0%; Score 300; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 3.3e-73;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 CATTGAGCTACAGAGAGACAGTACAGCATATGCTAGCATCTGCTGGACAGCAAA 60
DB  1 CATTGAGCTACAGAGAGACAGTACAGCATATGCTAGCATCTGCTGGACAGCAAA 60
QY  61 TGGTGGTGGGATCTTCTGACTGGAACACATGCTGAGCAAGTGGCCCTGAAAAGAGAGCTG 120
DB  61 TGGTGGTGGGATCTTCTGACTGGAACACATGCTGAGCAAGTGGCCCTGAAAAGAGAGCTG 120
QY  121 TGGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB  121 TGGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY  181 AACTAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB  181 AACTAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY  241 AAAAACTAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB  241 AAAAACTAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300

RESULT 2
US-08-690-011A-18
; Sequence 18, Application US/06690011A
; Patent No. 5914133
; GENETIC INFORMATION:
; APPLICANT: VINSON, Charles R.
; APPLICANT: KRYLOV, Dmitry
; TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN
; COMPLEXITY SPACE TO INACTIVATE THE FUNCTION OF A
; CELLULAR PROTEIN
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 445 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS WORD/MS DOS
; SOFTWARE: MacIn Seq, Version #1.0, Version #1.308
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690,011A
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION NUMBER: 60/001,654
; APPLICATION NUMBER: 60/001,654
; FILING DATE: 31-JUL-1995
; APPLICATION NUMBER: 60/018,496
; FILING DATE: 29-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Serunian, Leslie A.
; ADDRESS: 35-353
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: 2026-4199US1
; TELEPHONE: (212)758-4800
; INFORMATION FOR SEQ ID NO: 18:
; SEQ ID NO: 18: 300
; LENGTH: 294 base pairs
; TYPE: nucleic acid
; ORIGIN: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:

```

US-09-299-495F-16

Query Match 89.13; Score 267.2; DB 4; Length 281;

Best Local Similarity 98.91; Pred. No. 1e-64;

Matches 269; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 25 AQAAGCTATGGTATGACATGATCTGGACAGCAATGGTGGGATCTCGACTCGAC 84

Db 1 ATATATATATGGTATGACATGATCTGGACAGCAATGGTGGGATCTCGACTCGAC 60

QY 85 AAGCTGCTGGAGATGGCCCTGTGAAGACAGAGCTGGAAAGAGCGCGAAGACTGG 144

Db 61 AAGCTGCTGGAGATGGCCCTGTGAAGACAGAGCTGGAAAGAGCGCGAAGACTGG 120

QY 145 AGCAGGAAATGCTGAACTCGAGCGCGAGAGACAGCACTGAGAGCTCGCTT 204

Db 121 AGCAGGAAATGCTGAACTCGAGCGCGAGAGACAGCACTGAGAGCTCGCTT 180

QY 205 TCGAGCGAGATGCTGAACTCGAGCGCGAGAGAGAGAAATCGAGCTGCTGGAG 264

Db 181 TCGAGCGAGATGCTGAACTCGAGCGCGAGAGAGAGAAATCGAGCTGCTGGAG 240

QY 265 CTACCGAAGCTGCTCGAAGATCCCTGATTAA 296

Db 241 CTACCGAAGCTGCTCGAAGATCCCTGATTAA 272

RESULT 4

US-08-690-011A-16

; Sequence 16, Application US/08690011A

; Patent No. 5942433

; GENERAL INFORMATION:

; APPLICANT: KAYLOW, Dmitry

; TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN

; TITLE OF INVENTION: INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF A

; TITLE OF INVENTION: CELLULAR PROTEIN

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & PINNEGAN, L.L.P.

; STREET: 345 Park Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: GENESOURCE W.I.O., Version #1.308

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/690,011A

; FILING DATE: 31-JUL-1996

; PRIORITY DATE: 31-JUL-1995

; PRIOR APPLICATION DATA: 60/001,654

; FILING DATE: 31-JUL-1995

; APPLICATION NUMBER: 60/018,496

; FILING DATE: 23-MAY-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Serunian, Leslie A.

; REGISTRATION NUMBER: 35,353

; ADDRESS/LOCKER NUMBER: 2026-4199051

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)751-4800

; INFOFAX: (212)751-6849

; SEQUENCE CHARACTERISTICS: 16;

; LENGTH: 281 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: unknown

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-690-011A-16

Query Match 88.51; Score 265.6; DB 2; Length 281;

Best Local Similarity 98.51; Pred. No. 8.1e-64;

Matches 268; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 25 AQAAGCTATGGTATGACATGATCTGGACAGCAATGGTGGGATCTCGACTCGAC 84

Db 1 ATATATATATGGTATGACATGATCTGGACAGCAATGGTGGGATCTCGACTCGAC 60

QY 85 AAGCTGCTGGAGATGGCCCTGTGAAGACAGAGCTGGAAAGAGCGCGAAGACTGG 144

Db 61 AAGCTGCTGGAGATGGCCCTGTGAAGACAGAGCTGGAAAGAGCGCGAAGACTGG 120

QY 145 AGCAGGAAATGCTGAACTCGAGCGCGAGAGACAGCACTGAGAGCTCGCTT 204

Db 121 AGCAGGAAATGCTGAACTCGAGCGCGAGAGACAGCACTGAGAGCTCGCTT 180

QY 205 TCGAGCGAGATGCTGAACTCGAGCGCGAGAGAGAGAAATCGAGCTGCTGGAG 264

Db 181 TCGAGCGAGATGCTGAACTCGAGCGCGAGAGAGAGAAATCGAGCTGCTGGAG 240

QY 265 CTACCGAAGCTGCTCGAAGATCCCTGATTAA 296

Db 241 CTACCGAAGCTGCTCGAAGATCCCTGATTAA 272

RESULT 5

US-08-299-495F-14

; Sequence 14, Application US/09299495F

; Patent No. 6361368

; GENERAL INFORMATION:

; APPLICANT: VIKOV, Charles R.

; TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN

; TITLE OF INVENTION: INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF A

; TITLE OF INVENTION: CELLULAR PROTEIN

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORGAN & PINNEGAN, L.L.P.

; STREET: 345 Park Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10154-0053

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: MS WORD 97

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/299,495F

; FILING DATE: 26-APR-1999

; PRIOR APPLICATION DATA: 60/001,654

; FILING DATE: 31-JUL-1995

; APPLICATION NUMBER: 60/018,496

; FILING DATE: 23-MAY-1996

; APPLICATION NUMBER: 08/690,011

; ATTORNEY/AGENT INFORMATION:

; NAME: Serunian, Leslie A.

; REGISTRATION NUMBER: 35,353

; ADDRESS/LOCKER NUMBER: 2026-4199052

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)751-4800

; INFOFAX: (212)751-6849

; INFORMATION FOR SEQ ID NO. 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 324 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: unknown

; TOPOLOGY: linear

REGISTRATION NUMBER: 35,353

```

/ REFERENCE/DOCKET NUMBER: 2026-4199052
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212)751-6840
/ TELEFAX: (212)751-6849
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-059-299-495F-10      53.5%; Score 160.6; DB 4; Length 266;
Query Match
Best Local Similarity  37.0%; Pred. No. 3.9e-34;
Matches 160; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy  1  CATTGCTCTTACAGCGACGATGACACATCTTCTGCTACCTACCTGCTGCGACGCGAATG 62
Db    1  CATTGCTCTTACAGCGACGATGACACATCTTCTGCTACCTACCTGCTGCGACGCGAATG 60

Oy  61  TGGGTCTGGGATCTTCACTTGGACACGCTCTTGAGCATTTGGCTCTTGGACGAGAC 120
Db    61  TGGGTCTGGGATCTTCACTTGGACACGCTCTTGAGCATTTGGCTCTTGGACGAGAC 120

Oy  121  TGGAAAAGAGCGCGAGAGCTGTGAGCGAGAAAGACCTGAACTCTGAG 167
Db    121  TGGAAAAGAGCGCGAGAGCTGTGAGCGAGAAAGACCTGAACTCTGAG 167

/ RESULT 8
/ Sequence 10, Application US/08690011A
/ Patent No. 5942433
/ GENERAL INFORMATION:
/ APPLICANT: KEYLOV, Dmitry
/ TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN
/ TITLE OF INVENTION: INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF A
/ TITLE OF INVENTION: CELLULAR PROTEIN
/ NUMBER OF SEQUENCES: 60
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
/ STREET: 345 Park Avenue
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10154-0053
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ CURRENT STATUS: Patent in Release #1.0, Version #1.30B
/ FILING DATE: 31-JUL-1996
/ APPLICATION NUMBER: US/08/690,011A
/ PRIOR APPLICATION DATA: 60/001,654
/ FILING DATE: 31-JUL-1995
/ APPLICATION NUMBER: 60/018,496
/ NAME: Serunian, Leslie A.
/ ATTORNEY/AGENT INFORMATION:
/ REGISTRATION NUMBER: 35,353
/ REFERENCE/DOCKET NUMBER: 2026-4199051
/ TELEPHONE: (212)751-6840
/ TELEFAX: (212)751-6849
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 262 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-059-690-011A-12      44.5%; Score 133.4; DB 2; Length 262;
Query Match
Best Local Similarity  92.7%; Pred. No. 1.1e-27;

```



```

; CLASSIFICATION: 514
; PROTEIN APPLICATION DATA:
; PRT-SEQ: 125
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Monaco, Daniel A.
; REFERENCE/DOCKET NUMBER: 8321-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-8383
; TELEFAX: (215) 568-5449
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3565 base pairs
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-306-691B-44
Query Match 41.5%; Score 124.4; DB 1; Length 3565;
Best Local Similarity 99.2%; Pred. No. 7.4e-25;
Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US93-06251-20
Query Match 41.5%; Score 124.4; DB 5; Length 3565;
Best Local Similarity 99.2%; Pred. No. 7.4e-25;
Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 170 GGAGACGACCACTAGAGATGAGAGTCTCTTTGACGACGAGATTGCCACTCTCT 229
DB 2087 GGAGACGACCACTAGAGATGAGAGTCTCTTTGACGACGAGATTGCCACTCTCT 2146

QY 230 GAAGGAGAGAGAAAATAGAGTTCATCTCGAGCTCACGACCTGCTCCAGATGCC 289
DB 2147 GAAGGAGAGAGAAAATAGAGTTCATCTCGAGCTCACGACCTGCTCCAGATGCC 2206

QY 290 TGATTA 295
DB 2207 TGATTA 2212

RESULT 14
US-08-690-011A-32
; Sequence 20, Application US/08690011A
; Patent No. 6942433
; GENERAL INFORMATION:
; APPLICANT: VINSON, Charles R.
; ATTORNEY/AGENT INFORMATION:
; NAME: VINSON, Charles R.
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TITLE OF INVENTION: INTERACTION OF A PROTEIN-PROTEIN
; TITLE OF INVENTION: INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF A
; NUMBER OF SEQUENCES: 60
; CONSEQUENCE ACCESS: SCOTT, MURPHY & PRESSER
; ADDRESSER: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/690-011A
; FILING DATE: 29-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/001,654
; FILING DATE: 31-JUL-1995
; PRIORITY DATE: 31-JUL-1995
; APPLICATION NUMBER: 60/018,496
; FILING DATE: 29-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: VINSON, Charles R.
; REFERENCE/DOCKET NUMBER: 8321-8
; REGISTRATION NUMBER: 353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 758-4849
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 296 base pairs
; STRANDEDNESS: c acid
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-690-011A-32
Query Match 40.5%; Score 121.4; DB 2; Length 296;
Best Local Similarity 73.4%; Pred. No. 2.2e-24;
Matches 171; Conservative 0; Mismatches 56; Indels 6; Gaps 1;

```

QY 33 ATGCTAGCATGATCTGGTGGACAGCAATGGGTCTGGATCTCTGA-----CCTGGACAA 86
 Db 1 ATGCTAGCATGATCTGGTGGACAGCAATGGGTCTGGATCTCTGGCTGGCTGGACAA 60
 QY 87 CTGCTGAGGAAGTGGCTCGTGTAAACGAGAGAGTGGAAAAAGGCGGAGAGCTGGAG 146
 Db 61 CTGCTGAGGAAGTGGCTCGTGTAAACGAGAGAGTGGAAAAAGGCGGAGAGCTGGAG 120
 QY 147 CAGGAAAACCTGAACTCGAGCGGAGACAGACCACTGAGAGATGAGAGTCTGCTTTG 206
 Db 121 CAGGAAAACCTGAACTCGAGCGGAGACAGACCACTGAGAGATGAGAGTCTGCTTTG 206
 QY 207 CAGACGAGATGCGCAACTCTCGAAGGAGAGAAAACCTAGAGTTCATCT 259
 Db 181 CAGACGAGATGCGCAACTCTCGAAGGAGAGAAAACCTAGAGTTCATCT 259
 Db 181 CAGACGAGATGCGCAACTCTCGAAGGAGAGAAAACCTAGAGTTCATCT 233

RESULT 15
 ; Sequence 32, Application US/09299495F
 ; Patent No. 6361948
 ; GENERAL INFORMATION:
 ; APPLICANT: KENOV, Charles R.
 ; INVENTOR: KENOV, Charles R.
 ; TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN
 ; CELLULAR SURFACE TO INACTIVATE THE FUNCTION OF A
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; STREET: 345 Park Avenue
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10154-0053
 ; COMPUTER: IBM PC compatible
 ; MEDIA TYPE: ASCII
 ; OPERATING SYSTEM: MS WORD 97
 ; SOFTWARE: ASCII
 ; CURRENT FILE NAME: DATA
 ; APPLICATION NUMBER: US/09/299,495F
 ; FILING DATE: 26-Apr-1999
 ; PRIORITY NUMBER: 60/001,654
 ; FILING DATE: 31-Jul-1995
 ; APPLICATION NUMBER: 60/018,496
 ; FILING DATE: 29-May-1996
 ; PUBLICATION NUMBER: 09/690,011
 ; FILING DATE: 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Serunian, Leslie A.
 ; REGISTRATION NUMBER: 35,353
 ; PRACTICE ADDRESS:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212)758-4800
 ; TELEFAX: (212)751-6849
 ; INFORMATION: (212)751-6849
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 296 base pairs
 ; TYPE: nucleic acid
 ; STRATEGY: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Query Match 40.5%; Score 121.4; DB 4; Length 296;
 Best Local Similarity 73.4%; Pred. No. 2.2e-24;
 Matches 171; Conservative 0; Mismatches 56; Indels 6; Gaps 1;
 QY 33 ATGCTAGCATGATCTGGTGGACAGCAATGGGTCTGGATCTCTGA-----CCTGGACAA 86

Db 1 ATGCTAGCATGATCTGGTGGACAGCAATGGGTCTGGATCTCTGGCTGGCTGGACAA 60
 QY 87 CTGCTGAGGAAGTGGCTCGTGTAAACGAGAGAGTGGAAAAAGGCGGAGAGCTGGAG 146
 Db 61 CTGCTGAGGAAGTGGCTCGTGTAAACGAGAGAGTGGAAAAAGGCGGAGAGCTGGAG 120
 QY 147 CAGGAAAACCTGAACTCGAGCGGAGACAGACCACTGAGAGATGAGAGTCTGCTTTG 206
 Db 121 CAGGAAAACCTGAACTCGAGCGGAGACAGACCACTGAGAGATGAGAGTCTGCTTTG 206
 QY 207 CAGACGAGATGCGCAACTCTCGAAGGAGAGAAAACCTAGAGTTCATCT 259
 Db 181 CAGACGAGATGCGCAACTCTCGAAGGAGAGAAAACCTAGAGTTCATCT 233

Search completed, November 16, 2003, 00:58:53
 Job time : 51 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2003, 21:56:10 | Search time 1512 Seconds
8116.985 Million cell updates/sec

Title: US-10-059-720-18

Sequence: 1 CCAGTCACTACAGGAGAC.....CAGATCCCTGATTACGTT 300

Scoring table: IDENTITY_MUC
Gapop 10.0, Gapext 1.0

Searched: 2889711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 577422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 100%

Listing first 45 summaries

Database: GenBank

1: gb.ba.*

2: gb.hg.*

3: gb.in.*

4: gb.ov.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pr.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sts.*

13: gb.sts.*

14: gb.vi.*

15: gb.ba.*

16: gb.in.*

17: gb.in.*

18: em.in.*

19: em.in.*

20: em.in.*

21: em.in.*

22: em.in.*

23: em.in.*

24: em.in.*

25: em.in.*

26: em.in.*

27: em.in.*

28: em.in.*

29: em.in.*

30: em.in.*

31: em.in.*

32: em.in.*

33: em.in.*

34: em.in.*

35: em.in.*

36: em.in.*

37: em.in.*

38: em.in.*

39: em.in.*

40: em.in.*

41: em.in.*

42: em.in.*

43: em.in.*

44: em.in.*

45: em.in.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	300	100.0	300	6	AR202098 Sequence
2	267.2	89.1	281	6	AR202097 Sequence
3	179.4	59.8	324	6	AR202096 Sequence
4	133.4	44.5	262	6	AR202095 Sequence
5	133.4	44.5	262	6	AR202095 Sequence
6	130.8	43.6	1823	9	EC004490 Homo sapi
7	130.8	43.6	1818	9	AK097379 Homo sapi
8	130.8	43.6	1818	9	AK097379 Homo sapi
9	130.8	43.6	1818	9	AK097379 Homo sapi
10	130.2	43.4	273	6	AX014320 Sequence
11	124.4	41.5	700	9	AB022276 Homo sapi
12	124.4	41.5	700	9	AB022276 Homo sapi
13	124.4	41.5	700	9	AB022276 Homo sapi
14	124.4	41.5	700	9	AB022276 Homo sapi
15	124.4	41.5	700	9	AB022276 Homo sapi
16	124.4	41.5	700	9	AB022276 Homo sapi
17	124.4	41.5	700	9	AB022276 Homo sapi
18	124.4	41.5	700	9	AB022276 Homo sapi
19	124.4	41.5	700	9	AB022276 Homo sapi
20	124.4	41.5	700	9	AB022276 Homo sapi
21	124.4	41.5	700	9	AB022276 Homo sapi
22	124.4	41.5	700	9	AB022276 Homo sapi
23	124.4	41.5	700	9	AB022276 Homo sapi
24	124.4	41.5	700	9	AB022276 Homo sapi
25	124.4	41.5	700	9	AB022276 Homo sapi
26	124.4	41.5	700	9	AB022276 Homo sapi
27	124.4	41.5	700	9	AB022276 Homo sapi
28	124.4	41.5	700	9	AB022276 Homo sapi
29	124.4	41.5	700	9	AB022276 Homo sapi
30	124.4	41.5	700	9	AB022276 Homo sapi
31	124.4	41.5	700	9	AB022276 Homo sapi
32	124.4	41.5	700	9	AB022276 Homo sapi
33	124.4	41.5	700	9	AB022276 Homo sapi
34	124.4	41.5	700	9	AB022276 Homo sapi
35	124.4	41.5	700	9	AB022276 Homo sapi
36	124.4	41.5	700	9	AB022276 Homo sapi
37	124.4	41.5	700	9	AB022276 Homo sapi
38	124.4	41.5	700	9	AB022276 Homo sapi
39	124.4	41.5	700	9	AB022276 Homo sapi
40	124.4	41.5	700	9	AB022276 Homo sapi
41	124.4	41.5	700	9	AB022276 Homo sapi
42	124.4	41.5	700	9	AB022276 Homo sapi
43	124.4	41.5	700	9	AB022276 Homo sapi
44	124.4	41.5	700	9	AB022276 Homo sapi
45	124.4	41.5	700	9	AB022276 Homo sapi

ALIGNMENTS

Result	Sequence	300 bp	bp	DNA	linear	PAT	20-APR-2002
1	AR202098	18	18	from patent US 6361968			
2	AR202098	18	18	from patent US 6361968			
3	AR202098	18	18	from patent US 6361968			
4	AR202098	18	18	from patent US 6361968			
5	AR202098	18	18	from patent US 6361968			
6	AR202098	18	18	from patent US 6361968			
7	AR202098	18	18	from patent US 6361968			
8	AR202098	18	18	from patent US 6361968			
9	AR202098	18	18	from patent US 6361968			
10	AR202098	18	18	from patent US 6361968			
11	AR202098	18	18	from patent US 6361968			
12	AR202098	18	18	from patent US 6361968			
13	AR202098	18	18	from patent US 6361968			
14	AR202098	18	18	from patent US 6361968			
15	AR202098	18	18	from patent US 6361968			
16	AR202098	18	18	from patent US 6361968			
17	AR202098	18	18	from patent US 6361968			
18	AR202098	18	18	from patent US 6361968			
19	AR202098	18	18	from patent US 6361968			
20	AR202098	18	18	from patent US 6361968			
21	AR202098	18	18	from patent US 6361968			
22	AR202098	18	18	from patent US 6361968			
23	AR202098	18	18	from patent US 6361968			
24	AR202098	18	18	from patent US 6361968			
25	AR202098	18	18	from patent US 6361968			
26	AR202098	18	18	from patent US 6361968			
27	AR202098	18	18	from patent US 6361968			
28	AR202098	18	18	from patent US 6361968			
29	AR202098	18	18	from patent US 6361968			
30	AR202098	18	18	from patent US 6361968			
31	AR202098	18	18	from patent US 6361968			
32	AR202098	18	18	from patent US 6361968			
33	AR202098	18	18	from patent US 6361968			
34	AR202098	18	18	from patent US 6361968			
35	AR202098	18	18	from patent US 6361968			
36	AR202098	18	18	from patent US 6361968			
37	AR202098	18	18	from patent US 6361968			
38	AR202098	18	18	from patent US 6361968			
39	AR202098	18	18	from patent US 6361968			
40	AR202098	18	18	from patent US 6361968			
41	AR202098	18	18	from patent US 6361968			
42	AR202098	18	18	from patent US 6361968			
43	AR202098	18	18	from patent US 6361968			
44	AR202098	18	18	from patent US 6361968			
45	AR202098	18	18	from patent US 6361968			

REFERENCE 1 (bases 1 to 300)

AUTHORS Vinson,C.R. and Krylov,D.

TITLE Extension of a protein-protein interaction surface to inactive the

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

KEYWORDS

Pred. No. is the number of results predicted by chance to have a


```

FEATURES
  source      Location/Qualifiers
              /locus="Homo sapiens"
              /mol_type="Genomic DNA"
              /db_xref="taxon:9606"
BASE COUNT   780 a      954 c      978 g      853 t
ORIGIN
Query Match      41.5%; Score 124.4; DB 6; Length 3565;
Best Local Similarity 99.2%; Pred. No. 3.2e-19;
Matches 125; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY  170  GGAAGACGACCACTAGAGAGTGGAACTCTCTTTTCGAGCGGAGATTGCCAACCTCT 229
Db    |||||
QY  2087 GGAAGACGACCACTAGAGAGTGGAACTCTCTTTTCGAGCGGAGATTGCCAACCTCT 2146
Db    |||||
QY  230  GGAAGACGAGGAAAACCTAGAGTTCATCTTGGCGAGCTCACCAGCTGCTGCAGAGATCC 289
Db    |||||
QY  2147 GGAAGACGAGGAAAACCTAGAGTTCATCTTGGCGAGCTCACCAGCTGCTGCAGAGATCC 2206
Db    |||||
QY  290  TGATTA 295
Db    |||||
QY  2207 TGATGA 2212

```

Search completed: November 16, 2003, 00:35:55
 Job time : 1516 secs

LOCUS	AF103189	550 bp	linear	EST 22-MAR-2002
DEFINITION	DKFZ66862C2019.1 c66 (synonymy: hlc3) Homo sapiens cDNA clone			
ACCESSION	U070189.1 GI:15966544			
VERSION	AL070189.1 GI:15966544			
KEYWORDS	EST			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Theria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	Poustka A., Wellenreuther R., Mewes H.N., Weill B. and Wiemann S.).			
TITLE	Poustka A., Wellenreuther R., Mewes H.N., Weill B. and Wiemann S.).			
JOURNAL	U.S. biochad			
COMMENT	<p>Contact: Poustka A.J. Department Lehrfach Max-Planck-Institute for Molecular Genetics Im Neuenheimer Feld 267, D-69120 Heidelberg, Germany Tel.: +49-30-84131623 Fax: +49-30-84131128 Email: poustka@mpimg-berlin-dahlem.mpg.de</p> <p>This clone was sequenced within the context of the Human Genome Project. The clone from S. Wiemann, "Molecular Genome Analysis, German Cancer Research Center (DKFZ)", Email: s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg, Germany) within the GSC sequencing consortium of the German Genomes Project.</p> <p>No 1 sequence available. No 2 sequence available. Please contact DKFZ for more information. Berlin-Charlottenburg, Germany; Email: clone@dkfz.de</p>			

[illegible][illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OK protein - nucleic search, using frame plus p2n model

Run on: November 16, 2003, 02:28:12, Search time 271 Seconds

US-10-059-720-19
1161.230 Million cell updates/sec

File: 493
Perfect score: 493

Sequence: 1 MOYKDDKDHASHAGTQGM.....EKEKLEFILAHRACKPDI 97

Scoring table: BLOSUM62

Gapop 10.0, Xgapext 0.5

Gapop 10.0, Xgapext 0.5

Gapop 6.0, Xgapext 7.0

Delop 6.0, Delext 7.0

Searched: 2169961 seqs, 1634102185 residues

Total number of hits satisfying chosen parameters: 433922

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

-MODEL=frames.p2n model

-O=/cgm2_1/US070.spool/US10059720/runat_14112003_185001_17978/seq_query.fasta_1.263

-DB=Published Applications_MH-QFMT=fastcp-SUFFIX=ntds-MINMATCH=0.1

-TRANS=human40 cdi -LIST=45 -LOCAL=GEN-200 -THR SCORE=pcr -THR MAX=100

-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcr -NORM=ext -HEAPSIZE=500 -MINLEN=0

-MAXLEN=200000000 -USER=US10059720 -CGN_1_347 -runat_14112003_185001_17978

-CONSLOG -DEV TIMEOUT=120 -NASH TIMEOUT=30 -THRESH=0.1 -XGAPOP=10 -XGAPEXT=0.5

-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

1: /cgm2_6/prodata/1/pubna/US07_PUBCOMB.seq*

2: /cgm2_6/prodata/1/pubna/PCT_NEW_PUB.seq*

3: /cgm2_6/prodata/1/pubna/US06_NEW_PUB.seq*

4: /cgm2_6/prodata/1/pubna/US07_NEW_PUB.seq*

5: /cgm2_6/prodata/1/pubna/US07_NEW_PUB.seq*

6: /cgm2_6/prodata/1/pubna/PCTUS_PUBCOMB.seq*

7: /cgm2_6/prodata/1/pubna/US08_NEW_PUB.seq*

8: /cgm2_6/prodata/1/pubna/US09_NEW_PUB.seq*

9: /cgm2_6/prodata/1/pubna/US09A_PUBCOMB.seq*

10: /cgm2_6/prodata/1/pubna/US09B_PUBCOMB.seq*

11: /cgm2_6/prodata/1/pubna/US09C_PUBCOMB.seq*

12: /cgm2_6/prodata/1/pubna/US09D_PUBCOMB.seq*

13: /cgm2_6/prodata/1/pubna/US10_PUBCOMB.seq*

14: /cgm2_6/prodata/1/pubna/US10B_PUBCOMB.seq*

15: /cgm2_6/prodata/1/pubna/US10_NEW_PUB.seq*

16: /cgm2_6/prodata/1/pubna/US10_NEW_PUB.seq*

17: /cgm2_6/prodata/1/pubna/US06_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	Sequence 18, Appl
1	493	100.0	300	14	US-10-059-720-18

2	441	89.5	281	14	US-10-059-720-16	Sequence 16, Appl
3	350	71.0	324	14 <th>US-10-059-720-14</th> <th>Sequence 14, Appl</th>	US-10-059-720-14	Sequence 14, Appl
4	288	58.4	266	14 <th>US-10-059-720-13</th> <th>Sequence 13, Appl</th>	US-10-059-720-13	Sequence 13, Appl
5	241	48.9	219	14 <th>US-10-059-720-11</th> <th>Sequence 11, Appl</th>	US-10-059-720-11	Sequence 11, Appl
6	241	48.9	426	11 <th>US-09-818-995-33976</th> <th>Sequence 33976, A</th>	US-09-818-995-33976	Sequence 33976, A
7	241	48.9	2084	12 <th>US-10-007-9464-318</th> <th>Sequence 318, App</th>	US-10-007-9464-318	Sequence 318, App
8	241	48.9	2135	12 <th>US-09-871-332-8</th> <th>Sequence 332, Appl</th>	US-09-871-332-8	Sequence 332, Appl
9	241	48.9	2135	12 <th>US-09-871-332-8</th> <th>Sequence 332, Appl</th>	US-09-871-332-8	Sequence 332, Appl
10	236	47.9	2135	10 <th>US-09-860-352-7855</th> <th>Sequence 7855, AD</th>	US-09-860-352-7855	Sequence 7855, AD
11	235	47.7	435	11 <th>US-09-818-995-34766</th> <th>Sequence 34766, A</th>	US-09-818-995-34766	Sequence 34766, A
12	229	46.5	262	14 <th>US-10-059-720-12</th> <th>Sequence 12, Appl</th>	US-10-059-720-12	Sequence 12, Appl
13	216	43.8	273	14 <th>US-10-070-676-16</th> <th>Sequence 16, Appl</th>	US-10-070-676-16	Sequence 16, Appl
14	216	43.8	273	14 <th>US-10-070-676-16</th> <th>Sequence 16, Appl</th>	US-10-070-676-16	Sequence 16, Appl
15	216	43.8	415	10 <th>US-09-960-352-14906</th> <th>Sequence 14906, A</th>	US-09-960-352-14906	Sequence 14906, A
16	210	43.6	1176	13 <th>US-10-002-600-39</th> <th>Sequence 39, Appl</th>	US-10-002-600-39	Sequence 39, Appl
17	206	41.8	435	10 <th>US-09-860-352-7855</th> <th>Sequence 7855, AD</th>	US-09-860-352-7855	Sequence 7855, AD
18	206	41.8	435	10 <th>US-09-860-352-7855</th> <th>Sequence 7855, AD</th>	US-09-860-352-7855	Sequence 7855, AD
19	206	41.8	600	12 <th>US-10-024-386-12113</th> <th>Sequence 12113, A</th>	US-10-024-386-12113	Sequence 12113, A
20	206	41.8	642	9 <th>US-09-864-761-20191</th> <th>Sequence 20191, A</th>	US-09-864-761-20191	Sequence 20191, A
21	206	41.8	642	9 <th>US-09-864-761-20191</th> <th>Sequence 20191, A</th>	US-09-864-761-20191	Sequence 20191, A
22	206	41.8	2227	13 <th>US-10-002-600-36</th> <th>Sequence 36, Appl</th>	US-10-002-600-36	Sequence 36, Appl
23	206	41.8	2227	13 <th>US-10-002-600-36</th> <th>Sequence 36, Appl</th>	US-10-002-600-36	Sequence 36, Appl
24	206	41.8	3565	12 <th>US-09-871-319-649</th> <th>Sequence 649, App</th>	US-09-871-319-649	Sequence 649, App
25	206	41.8	3565	12 <th>US-09-871-319-649</th> <th>Sequence 649, App</th>	US-09-871-319-649	Sequence 649, App
26	206	41.8	3565	12 <th>US-09-871-319-649</th> <th>Sequence 649, App</th>	US-09-871-319-649	Sequence 649, App
27	206	41.8	3565	12 <th>US-09-871-319-649</th> <th>Sequence 649, App</th>	US-09-871-319-649	Sequence 649, App
28	206	41.8	3565	12 <th>US-09-871-319-649</th> <th>Sequence 649, App</th>	US-09-871-319-649	Sequence 649, App
29	206	41.8	3565	12 <th>US-09-871-319-649</th> <th>Sequence 649, App</th>	US-09-871-319-649	Sequence 649, App
30	206	41.8	3565	12 <th>US-09-871-319-649</th> <th>Sequence 649, App</th>	US-09-871-319-649	Sequence 649, App
31	186	37.7	300	13 <th>US-10-032-528-436</th> <th>Sequence 436, App</th>	US-10-032-528-436	Sequence 436, App
32	186	37.7	300	13 <th>US-10-032-528-436</th> <th>Sequence 436, App</th>	US-10-032-528-436	Sequence 436, App
33	186	37.7	300	13 <th>US-10-032-528-436</th> <th>Sequence 436, App</th>	US-10-032-528-436	Sequence 436, App
34	186	37.7	300	13 <th>US-10-032-528-436</th> <th>Sequence 436, App</th>	US-10-032-528-436	Sequence 436, App
35	186	37.7	300	13 <th>US-10-032-528-436</th> <th>Sequence 436, App</th>	US-10-032-528-436	Sequence 436, App
36	186	37.7	300	13 <th>US-10-032-528-436</th> <th>Sequence 436, App</th>	US-10-032-528-436	Sequence 436, App
37	186	37.7	300	13 <th>US-10-032-528-436</th> <th>Sequence 436, App</th>	US-10-032-528-436	Sequence 436, App
38	186	37.7	300	13 <th>US-10-032-528-436</th> <th>Sequence 436, App</th>	US-10-032-528-436	Sequence 436, App
39	186	37.7	300	13 <th>US-10-032-528-436</th> <th>Sequence 436, App</th>	US-10-032-528-436	Sequence 436, App
40	186	37.7	300	13 <th>US-10-032-528-436</th> <th>Sequence 436, App</th>	US-10-032-528-436	Sequence 436, App
41	186	37.7	300	13 <th>US-10-032-528-436</th> <th>Sequence 436, App</th>	US-10-032-528-436	Sequence 436, App
42	186	37.7	300	13 <th>US-10-032-528-436</th> <th>Sequence 436, App</th>	US-10-032-528-436	Sequence 436, App
43	186	37.7	300	13 <th>US-10-032-528-436</th> <th>Sequence 436, App</th>	US-10-032-528-436	Sequence 436, App
44	186	37.7	300	13 <th>US-10-032-528-436</th> <th>Sequence 436, App</th>	US-10-032-528-436	Sequence 436, App
45	173.5	35.2	290	14 <th>US-10-059-720-8</th> <th>Sequence 8, Appl</th>	US-10-059-720-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-10-059-720-18

Sequence 18, Application US/10059720

Publication No. US20030027134A1

GENERIC INFORMATION

APPLICANT: UNISON, Charles R.

INVENTOR: KAYLOV, Dmitry

TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN INTERACTION TO INACTIVATE THE FUNCTION OF A CELLULAR PROTEIN

NUMBER OF SEQUENCES: 64

CORRESPONDENCE ADDRESS:

ADDRESS: 2545 Park Avenue

CITY: New York

STATE: NY

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: GENSCAN, MS WORD 97

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/059,720

```

, FILING DATE: 29-Jan-2002
, PRIOR APPLICATION NUMBER: 60/001,654
, APPLICATION NUMBER: 60/001,654
, FILING DATE: 31-JUL-1995
, FILING DATE: 29-MAY-1996
, FILING DATE: 29-MAY-1996
, APPLICATION NUMBER: 08/690,011
, FILING DATE: 31-JULY-1996
, ATTORNEY/AGENT INFORMATION:
, NAME: Serutian, Leslie A.
, REGISTRATION NUMBER: 35,353
, REFERENCE/DOCKET NUMBER: 2026-4199US2
, TELEPHONE: (212)751-6849
, TELEFAX: (212)751-6849
, INFORMATION FOR SEQ ID NO: 18:
, SEQUENCE CHARACTERISTICS:
, TYPE: nucleic acid
, TOPOLOGY: linear
, STRANDNESS: unknown
, MOLECULE TYPE: DNA (genomic)
, SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-059-720-18
Alignment Scores:
Pred. No.: 4,346-52 Length: 300
Score: 493.00 Matches: 97
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-059-720-19 (1-97) x US-10-059-720-18 (1-300)
QY 1 MacAerTyrIleAspApeAspAspIleHisMetAlaSerMetThsGlyGlyGlnIleMet 20
Dd 3 ATCGCATACAGAGGACGACGACGACGACGATATGCGTGGACGACGAATG 62
QY 21 GLYATGAspProGluGluGluGluGluGluGluGluGluGluGluGluGlu 40
Dd 63 GGTGGGAGTCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 122
QY 41 GUKGKGLuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 60
Dd 123 GAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 182
QY 61 LantGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 80
Dd 183 CTAGAGATGATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 242
QY 81 IysGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 97
Dd 243 AATGAGTATGATCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 293

RESULT 2
US-10-059-720-16
; Sequence 16, Application US/10059720
; Publication No. US20030027314A1
; GENERAL INFORMATION:
; APPLICANT: KEYLOV, Dmitry
; APPLICANT: KEYLOV, Dmitry
; TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN
; INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF A
; CELLULAR PROTEIN
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: NEW YORK, NY
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053

```

```

, COMPUTER READABLE FORM:
, MEDIUM TYPE: Floppy disk
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: MS WORD 97
, SEQUENCE CHARACTERISTICS:
, TYPE: nucleic acid
, TOPOLOGY: linear
, STRANDNESS: unknown
, MOLECULE TYPE: DNA (genomic)
, SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-059-720-16
Alignment Scores:
Pred. No.: 1,016-45 Length: 281
Score: 441.00 Matches: 88
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 89.45% Indels: 0
DB: 14 Gaps: 0

US-10-059-720-19 (1-97) x US-10-059-720-16 (1-281)
QY 1 HisMetAlaSerMetThsGlyGlyGlnIleMetClyArgAspProAspLeuGlnIle 29
Dd 6 CATTGCTACACATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 65
QY 30 AlAGuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 49
Dd 66 GCTGAGAGTATGCTGAGTATGCTGAGTATGCTGAGTATGCTGAGTATGCTGAG 125
QY 50 GUAsnAlaGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 69
Dd 126 GAAAGAGTATGCTGAGTATGCTGAGTATGCTGAGTATGCTGAGTATGCTGAG 185
QY 70 ThsGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 89
Dd 186 ACAGAGTATGCTGAGTATGCTGAGTATGCTGAGTATGCTGAGTATGCTGAG 245
QY 90 ArgProAlaCysIleIleProAsp 97
Dd 246 GCACTCTGCTGAGTATCTGATCTGATCTGATCTGATCTGATCTGATCTG 269

RESULT 3
US-10-059-720-14
; Sequence 14, Application US/10059720
; Publication No. US20030027314A1
; GENERAL INFORMATION:
; APPLICANT: VINSON, Charles R.
; APPLICANT: KEYLOV, Dmitry
; TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN
; INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF A
; CELLULAR PROTEIN
; NUMBER OF SEQUENCES: 64

```



```

Qy 49 GlnGluuAnlAgLuLeuGluAluGluThrAspGluLeuGluAspProLeuLeuGluLeu 68
Db 121 CAGGAAACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 180
Qy 69 GlnThrGluLeuAlaLeuLeuGluGluLeuGluLeuGluLeuLeu 85
Db 181 CCGAAGAGAGTGGACAGCTGGAGGTGGATGACGACGACGACGACGACGACGACGAC 231

RESULT 10
US-09-960-352-7855
Sequence 7855, Application US/09960352
Publication No. US0020117119A1
EXEMPLAR INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Ningbing
APPLICANT: Byatt, John C.
APPLICANT: Wang, Xiangyan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 7855
TYPR: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 34-LTB188-026-Q1-EL-A10
US-09-960-352-7855
Alignment Scores:
Pred. No.: 2,54e-20 Length: 399
Score: 236.00 Matches: 57
Percent Similarity: 64.36 Conservative: 8
Best Local Similarity: 56.57% Mismatches: 18
Query Match: 47.87% Indels: 18
Gaps: 10

```

```

US-10-059-720-19 (1-97) X US-09-960-352-7855 (1-399)
Qy 11 MetAlaSerMetThrGlyVal-----GlnGlnMetGluValArgAspProLeuLeuGluGln 28
Db 104 ATGACACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 151
Qy 29 ArgAlaGluLeuAlaArgGluAlaGluGluGluGluGluGluGluGluGluGlu 48
Db 152 AGGTGAGAGAGTGTCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 211
Qy 49 GlnGluuAlaLeu-----GluLeuGluAla 56
Db 212 AGATGAGTGTGCGCCCAATGCCACCGACCGAGAGAGAGAGAGAGAGAGAGAGAGAG 271
Qy 57 GlnThrAspGluLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 76
Db 272 GAGCAGACGACCTGAGATGATGAGAGAGTGGCTGCTCCGAGAGAGAGATGCCATCTGCTG 331
Qy 77 TyroGluGluGluLeuGluPheLeuAlaAlaHisArgProAlaCysGluValLeu 96
Db 332 AAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 391
Qy 79 Asp 97
Db 382 GAT 394

```

```

RESULT 11
US-09-918-995-34766
Sequence 34766, Application US/09918995
Publication No. US20030073623A1
EXEMPLAR INFORMATION:
APPLICANT: Morgan, Charles R.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20441-756

```

```

CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
SEQUENCE ID NOS: 1-34766
NUMBER OF SEQ ID NOS: 34054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 34766
LENGTH: 435
ORGANISM: Homo sapiens
US-09-918-995-34766
Alignment Scores:
Pred. No.: 3,72e-20 Length: 435
Score: 235.00 Matches: 56
Percent Similarity: 64.65% Conservative: 8
Best Local Similarity: 56.57% Mismatches: 17
Query Match: 47.67% Indels: 18
Gaps: 3
US-10-059-720-19 (1-97) X US-09-918-995-34766 (1-435)
Qy 13 SerMetThrGlyVal-----GlnGlnMetGluValArgAspProLeuLeuGluGln 30
Db 12 ACATGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTGACCTG 59
Qy 31 GlnGluLeuAlaGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 50
Db 60 GACAGTATCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGATG 119
Qy 51 Anpba-----GluLeuGluAlaGluThr 58
Db 120 GCTCAGCCCAATGCCACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 179
Qy 59 ArgGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 78
Db 180 GACCACTGAGATGAGAGATGCTCTCTCCGAGAGAGATGCCATCTGCTGAGAG 239
Qy 79 TyroGluGluGluPheLeuAlaAlaHisArgProAlaCysGluValLeuProAsp 97
Db 240 AAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 296

RESULT 12
US-10-059-720-19
Sequence 12, Application US/10059720
Publication No. US200300231441
GENERAL INFORMATION:
APPLICANT: WARREN, Charles R.
TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN
INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF A
CELLULAR PROTEIN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM: disk
SOFTWARE: FASTA, IBM PC compatible
OPERATING SYSTEM: MS WORD 97
CURRENT APPLICATION DATA:
APPLICANT: WARREN, Charles R.
SEQUENCE NUMBER: US/10/059,720
FILING DATE: 29-Jan-2002
APPLICATION NUMBER: 60/001,654
PUBLICATION NO.: 200300231441
APPLICATION INVENTOR: 60/018,496
FILING DATE: 29-MAY-1996

```



```

Db 176 AACCTCTGAGAGGAGAGAGAAACATAGAGTTTCATCTCTGAGCTCTACCGACCTGCTCC 117
Qy 94 Lysleleprosep 97
Db 116 AAGATCCCTGAT 105

RESULT 15
US-09-960-352-14906
; Sequence 14906, Application US/09960352
; Patent No US002013713941
; ORIGINATOR: Warren, Wesley C.
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C
; APPLICANT: Kishimoto, Masaharu
; TITLE OF INVENTION: MUSCLE AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT PRIORITY NUMBER: 09/09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 14906
; LENGTH: 415
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 64-L7E188-010-Q1-E1-H12
US-09-960-352-14906

Alignment Scores:
Pred. No.: 7,678-18 Length: 415
Score: 216.00 Matches: 52
Percent Similarity: 51.3% Conservative: 12
Percent Identity: 43.8% Identical: 19
Query Match: 43.8% Indel: 18
DB: 10 Gaps: 3

US-10-059-720-19 (1-97) x US-09-960-352-14906 (1-415)
Qy 11 MetAlaserWethr-dlydly-----GlnGlnMetGlyArgpProlepLeuGln 28
Db 120 ATGAAAACCTGTGACGAGGAGGACGCTTCGAGCATTTGCGG-----AAGGC 167
Qy 29 ArgAlaGlnGluLeuAlaArgGluAndGluLeuGlyGluAlaGluLeuGln 48
Db 168 AAGGTAGACAGTTCTTCCCGAGAGGAGAAAGCGAGCTCCGAATGACGGAAT 227
Qy 49 GlnGluAlaAla-----GlnLeuGluAla 56
Db 228 AGGATGCTGCACCCNANTGCCCGAGACCGAGGAGGAGCTGACTGACACCTTCAATCG 287
Qy 57 GluThrAspGlnLeuGluAspGlySerAlaLeuGlnThrGluLeuAlaLeu 76
Db 288 GAGACGACCGCTACGATATGAGAGTTCAGTTCTCGAGAGATTCGCAATCTGCTG 347
Qy 77 LysGlyLysGluLeuGluPheLeuAlaAlaHisArgProbaLacGlyLeu 96
Db 348 AAGAGAAATGAAAACCTGATTTTCATCTCTGAGGCTCATGAGCTGCTGAGATCCCC 407
Qy 97 Asp 97
Db 408 GAT 410

```

Search completed: November 16, 2003, 03:46:31
Job time : 275 secs

ADDRESSEE: MORGAN & FINNIGAN, L.L.P.
 STREET: 345 Park Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10154-0053
 COMPANY NAME: MORGAN & FINNIGAN
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS WORD 97
 SOFTWARE: ASCII
 CURRENT ADDRESS:
 ADDRESSES: MORGAN & FINNIGAN, L.L.P.
 ADDRESS: 345 Park Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10154-0053
 APPLICATION NUMBER: US/09/299,495F
 FILING DATE: 26-Apr-1999
 PRIORITY NUMBER: 60/001,654
 FILING DATE: 31-JUL-1995
 APPLICATION NUMBER: 60/018,496
 FILING DATE: 29-MAY-1996
 PRIORITY NUMBER: 09/690,011
 FILING DATE: 31-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Serulian, Leslie A.
 REGISTRATION NUMBER: 35,353
 TELECOMMUNICATION INFORMATION: 204-4199082
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATIONAL NOTES:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 324 base pairs
 TYPE: nucleic acid
 STRANDNESS: unknown
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-299-995F-14

Alignment Scores:
 Prod. No.: 4,66-34 Length: 324
 Score: 350.00 Matches: 72
 Percent Similarity: 74.5% Conservative: 7
 Query Match: 10 Indels: 10
 DB: 4 Gaps: 2

US-10-059-720-19 (1-97) X US-09-299-495F-14 (1-324)

Qy 1 MetAaPvTlyvAspAspApvLyshiHwMetAlaSerMetThrGlyGlyGlnMet 20
 Db 3 AGGAGTCTCAGAGAGAGATGAGTGGCTGCGCCAAATGCCCAACCGAGAGGAGCTGACT 20
 Qy 21 GUYAGAspPvAspLeuGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 62
 Db 31 ATGAGTCTCAGAGAGAGATGAGTGGCTGCGCCAAATGCCCAACCGAGAGGAGCTGACT 62
 Qy 41 GUYAGAspPvAspLeuGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 119
 Db 63 GGTGGAGTCTCAGAGAGAGATGAGTGGCTGCGCCAAATGCCCAACCGAGAGGAGCTGACT 119
 Qy 41 GUYAGAspPvAspLeuGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 53
 Db 120 CAGAGAGAGAGATGAGTGGCTGCGCCAAATGCCCAACCGAGAGGAGCTGACT 179
 Qy 54 -----LeuGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 71
 Db 180 GATACATCTCAGAGAGAGATGAGTGGCTGCGCCAAATGCCCAACCGAGAGGAGCTGACT 239
 Qy 72 TleAlaMetLeuGlyGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 91
 Db 240 ATGCCCACTCTCAGAGAGAGATGAGTGGCTGCGCCAAATGCCCAACCGAGAGGAGCTGACT 299
 Qy 92 AlAcGlyMetLeuPvAsp 97
 Db 300 GCTTGCAGAGTCTCTGAT 317

RESULT 6

US-08-690-011A-14
 Sequence 14, Application US/08690011A
 Patent No. 5,946-34
 GENERAL INFORMATION:
 APPLICANT: VINSON, Charles R.
 APPLICANT: KRYLOV, Dmitry
 TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN
 INTERACTION: CHARACTERIZATION OF A PROTEIN
 TITLE OF INVENTION: CELLULAR PROTEIN
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSES: MORGAN & FINNIGAN, L.L.P.
 ADDRESS: 345 Park Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10154-0053
 COMPUTER TYPE: Floppy disk
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: MS WORD 97
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/690,011A
 FILING DATE: 31-JUL-1996
 PRIORITY NUMBER: 60/001,654
 FILING DATE: 31-JUL-1995
 PRIORITY NUMBER: 08/690,011
 FILING DATE: 29-MAY-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Serulian, Leslie A.
 REGISTRATION NUMBER: 35,353
 TELECOMMUNICATION INFORMATION: 204-4199081
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849 14:
 INFORMATIONAL NOTES:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 318 base pairs
 TYPE: nucleic acid
 STRANDNESS: unknown
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

Alignment Scores:
 Prod. No.: 5,946-34 Length: 318
 Score: 349.00 Matches: 72
 Percent Similarity: 74.5% Conservative: 7
 Query Match: 10 Indels: 10
 DB: 2 Gaps: 2

US-10-059-720-19 (1-97) X US-08-690-011A-14 (1-318)

Qy 1 MetAaPvTlyvAspAspApvLyshiHwMetAlaSerMetThrGlyGlyGlnMet 20
 Db 1 ATGAGTCTCAGAGAGAGATGAGTGGCTGCGCCAAATGCCCAACCGAGAGGAGCTGACT 60
 Qy 21 GUYAGAspPvAspLeuGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 40
 Db 61 GGTGGAGTCTCAGAGAGAGATGAGTGGCTGCGCCAAATGCCCAACCGAGAGGAGCTGACT 117
 Qy 41 GUYAGAspPvAspLeuGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 53
 Db 118 CAGAGAGAGAGATGAGTGGCTGCGCCAAATGCCCAACCGAGAGGAGCTGACT 177
 Qy 54 -----LeuGluGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 71
 Db 178 GATACATCTCAGAGAGAGATGAGTGGCTGCGCCAAATGCCCAACCGAGAGGAGCTGACT 237

Search completed: November 16, 2003, 02:57:53
Job time : 58 secs

DE	PCR template containing part of c-fos: c-fos (gSPRM).
EE	C-terminal modified protein, protein interaction detection;
EW	Protein analysis, protein-nucleic acid interaction; sg.
EX	Synthetic.
GS	Synthetic.
MO	MO200246395-Al.
PR	13-JUN-2002.
XX	07-DEC-2001; 2001MO-J210731.
PD	07-DEC-2000; 2000JP-0373105.
PF	07-DEC-2000; 2000JP-0373105.
XX	07-DEC-2000; 2000JP-0373105.
FA	(UNCL) UNCLIN (UNCLIN).

Yanagawa H, Doi N, Miyamoto E, Takashima H, Oyama R; WPT; 2002-500446/53.

Production of C-terminal modified proteins with nucleotide-linker containing modifying agents and translation templates, useful for studying protein-protein interaction in functional analysis of genes e.g. in genome projects

Example 2; Page 84; 95pp; Japanese.

The invention relates to an agent for modifying the C-terminal of a protein comprising an acceptor region with a group capable of binding to a protein through a transpeptidation reaction in a protein translation system. The agent is a nucleotide-linker, which is a nucleotide linked to a part of the acceptor region via a nucleoside linker. The modified proteins are useful for detecting protein interaction in a protein translation system. The agent is also useful for screening nucleic acid interaction in a high-throughput screening system.

CC genome function or outcome analysis. The modified proteins can be
CC conveniently and quickly applied in studying protein interactions, with
CC improved efficiency. AB95189-AB95225 represent PCR primers templates
CC used in examples of the invention.

XX Sequence 418 BP; 127 A; 91 C; 115 G; 95 T; 0 other;
SQ

Alignment Scores: 8 30e-23 418
Primer Length:

[illegible]

	QY	54	-----LeuGluIacIeUthrAspGlnLeuGluaspGluysrAalaLeuGln	69
202	AAATTCCTGGAGGAGCGAGACGAGAAAGATGUG--TGACGCCAGGTCCGCGGATTCGAGAGAGGAG		:::::	
	DB	262	CTGACAGATACACTCCAGCGGAGACAGATCACTTGAAGATGAGAAGTCTCGGTTCGC	321
	QY	70	TThCllleAlasnlLeuLeyzGluyluclyLysLeuclPhlelLeuAlahHis	89

1. *Journal of the American Medical Association*, 1997; 277: 103-107.

GenCov version 5.1.6
Copyright (C) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 16, 2003, 01:07:06 / Search time 2656 Seconds
(without alignments)
1385.465 Million cell updates/sec

Title: US-10-059-720-19

Perfect score: 493
Sequence: 1 MYKDDDDKHWSTGQQM.....REKLEFLAHPACKIPD 97

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 6.0, Ygapext 0.2
Zgapop 4.0, Zgapext 0.0
Delop 6.0, Delext 7.0

Searched: 288871 seqs, 2045411386 residues

Total number of hits satisfying chosen parameters: 577422

Maximum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0
Minimum Match 0
Listing first 45 summaries

Command line parameters: DBV=tbl
-O/cn2 1/GSPT0 spool/US10059720/runat 14112003 184959 17887/app query.fasta_1.263
-DB-GenEmbl1 -QPRV=fastap -SUFFIX=rgs -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MAXLEN=1000000000 -TRANS=want=0 -cd LIST=45
-CUTFWT=epco -NORM=ext -HSA812E=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10059720_@CN_1_1_5098 @runat 14112003 184959 17887 -NCPU=6 -ICPU=3
-NO_WAP -LARGOQUERY -NEG_SCORES=0 -MAXLEN=100 -LONGLOC
-FSAPEXT=10 -YGAPEXT=0.5 -DBLOC=6 -DBEXT=7
-FSAPEXT=10 -YGAPEXT=0.5 -DBLOC=6 -DBEXT=7

Database : GenEmbl1

- 1: gb-hsg1.*
- 2: gb-in.*
- 3: gb-hsg1.*
- 4: gb-om.*
- 5: gb-hsg1.*
- 6: gb-pat.*
- 7: gb-pat.*
- 8: gb-pat.*
- 9: gb-pat.*
- 10: gb-pat.*
- 11: gb-pat.*
- 12: gb-pat.*
- 13: gb-pat.*
- 14: gb-pat.*
- 15: gb-pat.*
- 16: gb-pat.*
- 17: gb-pat.*
- 18: gb-pat.*
- 19: gb-pat.*
- 20: gb-pat.*
- 21: gb-pat.*
- 22: gb-pat.*
- 23: gb-pat.*
- 24: gb-pat.*
- 25: gb-pat.*
- 26: gb-pat.*
- 27: gb-pat.*
- 28: gb-pat.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Accession	DB	ID	Description
1	493	100.0	300	6	AR202098 Sequence
2	441	89.5	281	6	AR202097 Sequence
3	441	89.5	281	6	AR202096 Sequence
4	288	58.4	266	6	AR202094 Sequence
5	274	55.6	418	6	BD169720 C-terminu
6	241	48.9	1823	9	EC091379 Homo sapi
7	241	48.9	1823	9	EC091379 Homo sapi
8	241	48.9	2084	6	AX587848 Sequence
9	241	48.9	2103	6	AX014320 Sequence
10	238	48.3	286	6	AX020305 Sequence
11	238	48.3	286	6	AX020305 Sequence
12	232	47.1	2116	10	RNC02088 Rat C-fos m
13	231	46.9	1146	10	AF033012 Cricetulu
14	231	46.9	3811	14	AF033012 Cricetulu
15	231	46.9	3811	14	AF033012 Cricetulu
16	230.5	46.8	2015	4	AF540379 Felis cat
17	229	46.5	262	6	AR202095 Sequence
18	229	46.5	4256	14	REM05014 Proteome of
19	229	46.5	4256	14	REM05014 Proteome of
20	219	44.4	1104	5	AF564329 Coturnix
21	219	44.4	1980	14	AC2N824 Avian trans
22	219	44.4	2253	5	CHRCPO2A Chicken c-f
23	219	44.4	2253	5	CHRCPO2A Chicken c-f
24	216	43.8	228	4	OAE515325 Ovis arie
25	216	43.8	273	6	AX098479 Sequence
26	216	43.9	381	3	AF069515 Bos tauru
27	216	43.9	381	3	AF069515 Bos tauru
28	207	42.0	1686	5	CCU81505 Cyprinus ca
29	207	42.0	6023	10	AF061881 Mesocric
30	206	41.8	414	4	ON15747 Ovis arie
31	206	41.8	414	4	ON15747 Ovis arie
32	206	41.8	760	9	AB022276 Homo sapi
33	206	41.8	3565	6	AX330284 Sequence
34	206	41.8	3565	6	AX330284 Sequence
35	206	41.8	3565	6	AX330284 Sequence
36	206	41.8	3565	6	196207 Sequence 44
37	206	41.8	3565	9	HSCFOS Human cellu
38	206	41.8	3673	10	MUSPOS Mouse c-fos
39	206	41.8	3673	10	MUSPOS Mouse c-fos
40	206	41.8	3967	6	BD078052 JMK3-cont
41	206	41.8	3967	10	WACFOS
42	206	41.8	4200	4	SSC132510 Sus scrofa
43	206	41.8	4200	4	SSC132510 Sus scrofa
44	206	41.8	6210	6	AX661628 Sequence
45	206	41.8	6210	9	HUMFOS Human fos p

ALIGNMENTS

RESULT 1

AR202098 AR202098 300 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 14 from patent US 6361968.
 ACCESSION AR202098
 VERSION AR202098.1 GI:20256637
 KEYWORDS Unknown.
 SOURCE ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 300)
 AUTHORS Vinson C.R. and Krylov D.
 TITLE Extension of a protein-protein interaction surface to inactive the function of a cellular protein
 JOURNAL
 FEATURES Patent: US 6361968-A 16 26-MAR-2002;
 Location/Qualifiers
 source 1..324
 /organism="unknown"
 BASE COUNT 96 a 68 c 89 g 47 t
 ORIGIN
 Alignment Scores: 6.76e-39 Length: 300
 Pred. No.: 300
 Score: 493.00 Matches: 97
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 97
 Indels: 0
 Gaps: 0
 DB:

US-10-059-720-19 (1-97) x AR202098 (1-300)

Qy 1 MetAspTyrIysAspAspAspIysHisMetAlaSerMetThrGlyGlyGlnGlnMet 20
 Db 3 ATGACATCTACAGCGACGAGTACGACACGCTTGGCTACGATCTGTGTGACGACGATG 62

Qy 21 GlyAspAspProLeuLeuGlnGlnArgAlaGluGluLeuAlaArgLeuGluGln 40
 Db 63 GGTGGGATCTCTGATCTGGACAGCGTGTGAGGACTGTGCCCTCGTAAACAGAGAGCTG 122

Qy 41 GlutylsAlaGluGluLeuGluGlnGluAlaGluLeuAlaGluLeuAlaGluThrArgin 60
 Db 123 GAAAGAGGCGCCGAGAGCTGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 182

Qy 61 LeuAlaGluGluGluSerAlaGluGlnThrGluAlaLeuLeuLeuLeuLeuGlu 80
 Db 183 CTGAGAGATGAGAGAGCTCTCTTTTGCACACGAGAGATGCCACACTCTCTGTAAGAGAGAA 242

Qy 81 LysLeuGluGluThrLeuAlaHisArgProbaCysGlyIleProbaPep 97
 Db 243 AACTAGAGTTCATCTGTGCGAGCTACCGACCTGCTCTCGAAGTCTCTTCAT 293

RESULT 2
 AR202097 AR202097 281 bp DNA linear PAT 20-APR-2002
 LOCUS Sequence 16 from patent US 6361968.
 ACCESSION AR202097
 VERSION AR202097.1 GI:20256635
 KEYWORDS Unknown.
 SOURCE ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 281)
 AUTHORS Vinson C.R. and Krylov D.
 TITLE Extension of a protein-protein interaction surface to inactive the function of a cellular protein
 JOURNAL
 FEATURES Patent: US 6361968-A 16 26-MAR-2002;
 Location/Qualifiers
 source 1..281
 /organism="unknown"
 BASE COUNT 90 a 82 c 81 g 48 t
 ORIGIN
 Alignment Scores: 5.73e-34 Length: 281
 Pred. No.: 281

US-10-059-720-19 (1-97) x AR202097 (1-281)

Qy 10 HisMetAlaSerMetThrGlyGlyGlnGlnMetGlyAspAspProLeuGlnGlnArg 29
 Db 6 CATATGCTGTGATGATCTGTGTGACGACAAATGCTGTGGATCTCTGACTTGGAAAGACT 65

Qy 30 AlaGluGluLeuAlaGluGluGluGluGluGluGluGluGluGluGluGluGln 49
 Db 66 GTTGAGAGATGCTGCTCGTCAAAAGAGAGAGCTGAGAAAGAGAGAGAGAGAGAGAGAG 125

Qy 50 GluAlaGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 69
 Db 136 GAAACCTGCTGATCTGCGAGCGAGGACGACACTGATGATGATGATGATGATGATGATG 185

Qy 70 ThrGluAlaLeuLeuLeuGluGluGluGluGluGluGluGluGluGluGluGluGln 89
 Db 186 ACCGAGTGTCCACTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 245

Qy 90 ArgProbaCysGlyIleProbaPep 97
 Db 246 CACTCTCTCTGCGAAGTCTCTTCAT 269

RESULT 3
 AR202096 AR202096 324 bp DNA linear PAT 20-APR-2002
 LOCUS Sequence 14 from patent US 6361968.
 ACCESSION AR202096
 VERSION AR202096.1 GI:20256635
 KEYWORDS Unknown.
 SOURCE ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 324)
 AUTHORS Vinson C.R. and Krylov D.
 TITLE Extension of a protein-protein interaction surface to inactive the function of a cellular protein
 JOURNAL
 FEATURES Patent: US 6361968-A 14 26-MAR-2002;
 Location/Qualifiers
 source 1..324
 /organism="unknown"
 BASE COUNT 109 a 71 c 93 g 51 t
 ORIGIN
 Alignment Scores: 3.16e-25 Length: 324
 Pred. No.: 324
 Score: 245.00 Matches: 72
 Percent Similarity: 72.50%
 Best Local Similarity: 67.92%
 Query Match: 70.95%
 Indels: 10
 Gaps: 2
 DB:

US-10-059-720-19 (1-97) x AR202096 (1-324)

Qy 1 MetAspTyrIysAspAspAspIysHisMetAlaSerMetThrGlyGlyGlnGlnMet 20
 Db 3 ATGACATCTACAGCGACGAGTACGACACGCTTGGCTACGATCTGTGTGACGACGATG 62

Qy 21 GlyAspAspProLeuLeuGlnGlnArgAlaGluGluLeuAlaArgLeuGluGln 40
 Db 63 GGTGGGATCTCTGATCTGGACAGCGTGTGAGGACTGTGCCCTCGTAAACAGAGAGCTG 119

Qy 41 GlutylsAlaGluGluGluGluGlnGluAlaGluLeuAlaGluLeuAlaGluThrArgin 60
 Db 120 CGAAGGAGAGAGAGATGAGTGTGCGAGCTGCGCAATGCGCAACCGAGAGAGAGAGAGAG 179

Qy 54 -----LeuGluAlaGluThrArginLeuGluAspGluIysSerAlaLeuGluGln 71

Score: 441.00 Matches: 88
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 89.45%
 Indels: 0
 Gaps: 0
 DB:

